

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 08:16:23 : Search time 4804 Seconds

(without alignments)
16756.528 Million cell updates/sec

US-10-054-680-1

Perfect score: 2766
Sequence: 1 atggcgtggttaagttgca.....gtcatcaaggggttctaa 2766

Scoring table:
IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database: GenBank
Updating 100845 summaries

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: gb_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vt:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2766.4	99.9	2966	6	AX480881 Sequence
2	2766.2	99.8	2792	6	AX476818 Sequence
3	2763.4	99.0	2837	6	AX476820 Sequence
4	2763.4	98.8	2781	6	AX299471 Sequence
5	2657.6	96.1	2840	6	AX300652 Sequence
6	2352.4	85.0	4854	10	RNU52420
7	2290.2	82.8	3435	10	AF453257
8	1786.4	64.6	2534	9	HSNCX22
9	1784.8	64.5	126512	6	AX476820
10	1784.8	64.5	145118	9	AF508982
11	1784.8	64.5	146055	2	AC009607
12	1784.8	64.5	206256	2	CNS01867
13	1546.4	55.9	186831	2	AC124384
14	1544	55.8	1784	10	AF321404
15	1326.4	48.0	2814	9	AF108389
16	1326.4	48.0	2965	9	AF107593
17	1316.8	47.6	3292	4	OCU52655
18	1302.6	47.1	2805	10	AF109163
19	1301	47.0	2805	10	AF109166
20	1294.4	46.8	3037	10	RNSCEA1
21	1277	46.2	4282	9	AB029010
22	1270.8	45.9	3004	10	RNU08141
23	1259.8	45.5	2773	10	AF503502
24	1257.4	45.5	2883	9	AF108388
25	1257.4	45.5	3002	9	AF128524
26	1232	44.5	2874	10	AF109164
27	1230.4	44.5	3303	10	RNU04933
28	1227.8	44.4	4087	4	BOVECHANG
29	1227.8	44.4	4087	6	AX360315
30	1227	44.4	3126	10	RNSCEA2
31	1219.6	44.1	3199	4	DOGSNCE
32	1216.6	44.0	2889	10	AY033398
33	1212.2	43.8	3150	4	CATSCC
34	1208.8	43.7	3184	9	HUYNACAA
35	1208.8	43.7	3250	9	HUYNAC
36	1201	43.4	3168	10	CEP04955
37	1196	43.2	2910	10	AF109165
38	1186.4	42.9	3155	10	RNSCEX
39	1180.8	42.7	3302	5	AF175313
40	1171	42.3	3180	10	MMU70033
41	1079.2	39.0	3344	10	AF004666
42	922	33.3	3670	9	HS802925
43	878.4	31.8	2756	9	AK096553
44	816.4	29.5	4096	3	LOC93214
45	797.8	28.8	1920	4	FCNCX154

ALIGNMENTS

RESULT 1	LOCUS	AX480881	2966 bp	DNA	linear	PAT 12-AUG-2002
DEFINITION	Sequence	41 from Patent WO/2004/019.				
ACCESSION	AX480881					
VERSION	AX480881.1	GI:22217538				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1					
AUTHORS	Lee, E. A., Baughn, M. R., Yue, H., Ding, L., Raumann, B. E., Hafealla, A. J., Khan, F. A., Nguyen, D. B., Elliott, V. S., Ramkumar, J., Walla, N. K., Ison, C. H., Lu, Y., Gandhi, A. R., Warren, B. A., Duggan, B. M.,					

Tribouley, C. M., Burford, N., Lu, D. A., Lal, P. G., Yao, M. G., Xu, Y.,
 Bruns, C. M., Thangavelu, K., Swarnakar, A., Tang, Y. T., Azimzai, Y.,
 Thornton, M., Arizizu, C. and Policky, J. L.
 Transporters and ion channels
 Patent: WO 0246415-A 41 13-JUN-2002;
 Incyte Genomics, Inc. (US)

FEATURES
 source
 1. .2966
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /note="Incyte ID No: 5923789CB1"

BASE COUNT 692 a 725 c 809 g 740 t
 ORIGIN

Query Match 99.9%: Score 2764.4; DB 6; Length 2966;
 Best Local Similarity 100.0%: Pred. No. 0;
 Matches 2765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATGGCGTGTAAAGTTGACGCTCTGACCTCTGCTCCATTTTGGGCTGTTACC 60
 DB 201 ATGGCGTGTAAAGTTGACGCTCTGACCTCTGCTCCATTTTGGGCTGTTACC 260
 Y 61 TTTGTGCTCTCCGTAATGGCTCTGACGAGAGGCTGGCTCAGGAGAGCTGCAAGC 120
 DB 261 TTTGTGCTCTCCGTAATGGCTCTGACGAGAGGCTGGCTCAGGAGAGCTGCAAGC 320
 OY 121 ACAGGCGAAGCAATGAGTCTGTTACAGGCTGATCGAGCTGCAAGAGAGGCTGCTCTG 180
 DB 321 ACAGGCGAAGCAATGAGTCTGTTACAGGCTGATCGAGCTGCAAGAGAGGCTGCTCTG 380
 OY 181 CCAATCTGTACCCGAGAACCTTCCCTTGGGACAAGATTGCCAGGGTCAATTGTCTAT 240
 DB 381 CCAATCTGTACCCGAGAACCTTCCCTTGGGACAAGATTGCCAGGGTCAATTGTCTAT 440
 OY 241 TTTGTGCGCCGATATACATGTTCTGCGGCTGTCATCATCTGTCACCGCTTATGGA 300
 DB 441 TTTGTGCGCCGATATACATGTTCTGCGGCTGTCATCATCTGTCACCGCTTATGGA 500
 OY 301 TCTATTGAGTCATCACCTCTCAAGAGAGGAGTGACAAATTAAGAAACCAATGAGAA 360
 DB 501 TCTATTGAGTCATCACCTCTCAAGAGAGGAGTGACAAATTAAGAAACCAATGAGAA 560
 OY 361 ACCAGCAACCACTATTGGGCTCTGGAATGAACCTGTCTCCAACTGACCTTATGGCC 420
 DB 561 ACCAGCAACCACTATTGGGCTCTGGAATGAACCTGTCTCCAACTGACCTTATGGCC 620
 OY 421 CTGGGCTCTGCTGCTGAGATACCTCTCTTAATTAGAGGTGTGGTCATGGGTTG 480
 DB 621 CTGGGCTCTGCTGCTGAGATACCTCTCTTAATTAGAGGTGTGGTCATGGGTTG 680
 OY 481 ATTGCTGTGATCTGGAGCTTCTACCATTTAGAGAGTGACAGCTTCAACATGTTCATC 540
 DB 681 ATTGCTGTGATCTGGAGCTTCTACCATTTAGAGAGTGACAGCTTCAACATGTTCATC 740
 OY 541 ATCATTTGGCATCTGTCTACGTGATCCAGAGCGAGAGACTGCGAAGATCAAGCATCTA 600
 DB 741 ATCATTTGGCATCTGTCTACGTGATCCAGAGCGAGAGACTGCGAAGATCAAGCATCTA 800
 OY 601 CGAGCTCTTCTTCATCACCGGCTTGGAGTATCTTTGCTACATCTGGCTATATGATT 660
 DB 801 CGAGCTCTTCTTCATCACCGGCTTGGAGTATCTTTGCTACATCTGGCTATATGATT 860
 OY 661 CTGGCAGCTCTTCTCCCTGGTGTGTCAGAGTTTGGAGAGGCTCTCAGCTCTTCTTC 720
 DB 861 CTGGCAGCTCTTCTCCCTGGTGTGTCAGAGTTTGGAGAGGCTCTCAGCTCTTCTTC 920
 OY 721 TTTTCACTGTGTCTCTTCTGGGCTGGGTGAGATTAAGAGACTGCTCTTCAAAATAC 780
 DB 921 TTTTCACTGTGTCTCTTCTGGGCTGGGTGAGATTAAGAGACTGCTCTTCAAAATAC 980
 OY 781 ATGCACAAAAGTACCGCAGACAAACACCGAGGAATTATCATAGAGACAGAGGTGAC 840
 DB 981 ATGCACAAAAGTACCGCAGACAAACACCGAGGAATTATCATAGAGACAGAGGTGAC 1040

OY 841 CACCTTAAGGCGCATTTGAGATGATGGGAAAATGATGAATTCCTCTTTAGATGGGAA 900
 DB 1041 CACCTTAAGGCGCATTTGAGATGATGGGAAAATGATGAATTCCTCTTTAGATGGGAA 1100
 OY 901 CTGGTGCCCTCGAAGGGAAGAGTGTAGTCCCGCAGAGAGATGATCCGATTCCTC 960
 DB 1101 CTGGTGCCCTCGAAGGGAAGAGTGTAGTCCCGCAGAGAGATGATCCGATTCCTC 1160
 OY 961 AAGATGTGAAGCAAAAACCCAGAGAGACTTATATACAGTGGTGGATGGCCAAAT 1020
 DB 1161 AAGATGTGAAGCAAAAACCCAGAGAGACTTATATACAGTGGTGGATGGCCAAAT 1220
 OY 1021 TACTATGCTCTTTTCCACCAAGAGAGCGGCGCTTCTACCGTATCCAGGCACTGCT 1080
 DB 1221 TACTATGCTCTTTTCCACCAAGAGAGCGGCGCTTCTACCGTATCCAGGCACTGCT 1280
 OY 1081 ATGATGACTGTGCGAGCAATATCTGAGAAACATGACAGAACCAAGCAAGAGGCC 1140
 DB 1281 ATGATGACTGTGCGAGCAATATCTGAGAAACATGACAGAACCAAGCAAGAGGCC 1340
 OY 1141 TCCAGCATGAGCGAGGTCACACCGATGAGCTGAGACTTATTCAGAGTCTTCTT 1200
 DB 1341 TCCAGCATGAGCGAGGTCACACCGATGAGCTGAGACTTATTCAGAGTCTTCTT 1400
 OY 1201 GACCATGTTCTTACCACTGCTGAGAACCTGCGGCTTACTCTGACAGTGTGAGG 1260
 DB 1401 GACCATGTTCTTACCACTGCTGAGAACCTGCGGCTTACTCTGACAGTGTGAGG 1460
 OY 1261 AAGGGGAGACATGTCAAAAGCACTATATGTGACTCAAAAACAGAGATGCTTCC 1320
 DB 1461 AAGGGGAGACATGTCAAAAGCACTATATGTGACTCAAAAACAGAGATGCTTCC 1520
 OY 1321 AATGACAGGGCTGACTATGAGTTTACAGAGGCAAGGTTGTCGAAGCCAGAGAGAC 1380
 DB 1521 AATGACAGGGCTGACTATGAGTTTACAGAGGCAAGGTTGTCGAAGCCAGAGAGAC 1580
 OY 1381 CAGAGAGAGTCTTCCGCTGGGCAATATGATGAGACACTTTTGGAGAGATGAACAATTC 1440
 DB 1581 CAGAGAGAGTCTTCCGCTGGGCAATATGATGAGACACTTTTGGAGAGATGAACAATTC 1640
 OY 1441 TTTGTAAAGTTGAGCAATGTCCGATAGAGAGAGCAGCCAGAGAGAGGATGCTTCCA 1500
 DB 1641 TTTGTAAAGTTGAGCAATGTCCGATAGAGAGAGCAGCCAGAGAGAGGATGCTTCCA 1700
 OY 1501 GCAATATTCAACAGTCTTCCCTTGGCTCGGGCTGCTCTACCTCCCTTGTGGCCACA 1560
 DB 1701 GCAATATTCAACAGTCTTCCCTTGGCTCGGGCTGCTCTACCTCCCTTGTGGCCACA 1760
 OY 1561 GTTACCATCTTGGATGATGACATGACAGGCACTTCACTTTGAAATGTGATACATTCAT 1620
 DB 1761 GTTACCATCTTGGATGATGACATGACAGGCACTTCACTTTGAAATGTGATACATTCAT 1820
 OY 1621 GTGAGTGAAGATATGTGTATTATGAGAGTCAAGGTTTGGGAGATCAAGTGGCCGGGT 1680
 DB 1821 GTGAGTGAAGATATGTGTATTATGAGAGTCAAGGTTTGGGAGATCAAGTGGCCGGGT 1880
 OY 1681 ACAGTATCTGCCCTTTAGAGCAGTGAAGGAGCAGCAAGGAGTGGCGGTGAGGACTTT 1740
 DB 1881 ACAGTATCTGCCCTTTAGAGCAGTGAAGGAGCAGCAAGGAGTGGCGGTGAGGACTTT 1940
 OY 1741 GAAGACACATATGGGAGTTGGAATTCMAAATGATGAACCTGTGAAMACCATTAAGGTTT 1800
 DB 1941 GAAGACACATATGGGAGTTGGAATTCMAAATGATGAACCTGTGAAMACCATTAAGGTTT 2000
 OY 1801 AAAATAGTACATGAGAGCAATACGAAAGCAGAGAAATTTCTTCACTGCTTGGTGA 1860
 DB 2001 AAAATAGTACATGAGAGCAATACGAAAGCAGAGAAATTTCTTCACTGCTTGGTGA 2060
 OY 1861 CCGAAATGATGAGAGCTGGAATATCATGATGTACAGACAGAGAGCTGACTATGGAAGA 1920
 DB 2061 CCGAAATGATGAGAGCTGGAATATCATGATGTACAGACAGAGAGCTGACTATGGAAGA 2120

```

Oy 1921 GAGGAGCCCAAGAGATAGACAGATGGGAAGCCAGTATGGGTGAACCCCAACTA 1980
    |||||
Db 2121 GAGGAGGCCAAGAGATAGACAGATGGGAAGCCAGTATGGGTGAACCCCAACTA 2180
Oy 1981 GAAATGATCATTTGAAGAGTCTTATGATTTCAAGACTACGGGTGACAACTGATCAAGA 2040
    |||||
Db 2181 GAAGTATCATTTGAAGAGTCTTATGATTTCAAGACTACGGGTGACAACTGATCAAGA 2240
Oy 2041 ACAAACTGGGCTTGGTGGGGAACCAATCTGGAGGAGACAGTTCATGAGGCCAATC 2100
    |||||
Db 2241 ACAAACTGGGCTTGGTGGGGAACCAATCTGGAGGAGACAGTTCATGAGGCCAATC 2300
Oy 2101 ACCGTAGTGCAGCAGGAGGATGAGATGATGAATCCGGGAGAGAGAGCGTCCCTCC 2160
    |||||
Db 2301 ACCGTAGTGCAGCAGGAGGATGAGATGATGAATCCGGGAGAGAGAGCGTCCCTCC 2360
Oy 2161 TGGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2220
    |||||
Db 2361 TGGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2420
Oy 2221 CCCCCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2280
    |||||
Db 2421 CCCCCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2480
Oy 2281 ATGCTACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
    |||||
Db 2481 ATGCTACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2540
Oy 2341 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
    |||||
Db 2541 GATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2600
Oy 2401 AGCAAGGCTGGGCTCCAGGATGATGATGATGATGATGATGATGATGATGATGATG 2460
    |||||
Db 2601 AGCAAGGCTGGGCTCCAGGATGATGATGATGATGATGATGATGATGATGATGATG 2660
Oy 2461 AGCAAGGCTGGGCTCCAGGATGATGATGATGATGATGATGATGATGATGATGATG 2520
    |||||
Db 2661 AGCAAGGCTGGGCTCCAGGATGATGATGATGATGATGATGATGATGATGATGATG 2720
Oy 2521 TGGGCTCTGACAGGAGAGAGATTCACAGTGTGGCCGACACTGGCTTTCCTGAC 2580
    |||||
Db 2721 TGGGCTCTGACAGGAGAGAGATTCACAGTGTGGCCGACACTGGCTTTCCTGAC 2780
Oy 2581 CTTTACACATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640
    |||||
Db 2781 CTTTACACATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2840
Oy 2641 CTGGGAGGAGAGCTTGTGGGCCCCGCTGGCTGACAGCTGACCAAAATGATGCTTGTG 2700
    |||||
Db 2841 CTGGGAGGAGAGCTTGTGGGCCCCGCTGGCTGACAGCTGACCAAAATGATGCTTGTG 2900
Oy 2701 AGCTGTGGCTCTCTACATCTTGTGGCAGACTAGAGGCTTATGCTATCAAGGGG 2760
    |||||
Db 2901 AGCTGTGGCTCTCTACATCTTGTGGCAGACTAGAGGCTTATGCTATCAAGGGG 2960
Oy 2761 TTCTAA 2766
    |||||
Db 2961 TTCTAA 2966

```

```

RESULT 2
AX476818 2782 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 1 from Patent W00233086.
ACCESSION AX476818
VERSION AX476818.1 GI:22216098
KEYWORDS
SOURCE
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1

```

```

AUTHORS Merkulov, G.V., Ketchum, K.A., Shao, W., Yan, C., di Francesco, V., and
         Beasley, E.M.
TITLE Isolated human transporter proteins, nucleic acid molecules
        encoding human transporter proteins, and uses thereof
JOURNAL Patent: WO 0233086-A 1 25-Apr-2002;
        PE Corporation (NY) (US)
FEATURES
        source
            1..2782
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT 655 a 685 c 766 g 676 t
ORIGIN
Query Match 99.8%; Score 2761.2; DB 6; Length 2782;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 ATGGCGTGGTTAAGTTGAGCTGACGCTCTACACTCTGCTTCCATTTTGGCTGTAC 60
    |||||
Db 10 ATGGCGTGGTTAAGTTGAGCTGACGCTCTACACTCTGCTTCCATTTTGGCTGTAC 69
Oy 61 TTTGTGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
    |||||
Db 70 TTTGTGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 129
Oy 121 ACAGGCGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
    |||||
Db 130 ACAGGCGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 189
Oy 181 CCAATCTGGTACCCGAGAACCTTCCCTTGGGAGCAAGATTTGCCAGGGTCAATTGCTAT 240
    |||||
Db 190 CCAATCTGGTACCCGAGAACCTTCCCTTGGGAGCAAGATTTGCCAGGGTCAATTGCTAT 249
Oy 241 TTTGTGCCCCATATATATATATATATATATATATATATATATATATATATATATAT 300
    |||||
Db 250 TTTGTGCCCCATATATATATATATATATATATATATATATATATATATATATATAT 309
Oy 301 TCTATTGAAGTATACCTCTCAAGAGAGGAGGATTAAGAAACCAATGAGAGA 360
    |||||
Db 310 TCTATTGAAGTATACCTCTCAAGAGAGGAGGATTAAGAAACCAATGAGAGA 369
Oy 361 ACCAGACAAACCAATTTGGGCTTGAATGAAGTGTCTCCAACTGACCTTATGGCC 420
    |||||
Db 370 ACCAGACAAACCAATTTGGGCTTGAATGAAGTGTCTCCAACTGACCTTATGGCC 429
Oy 421 CTGGGTTCTCTGCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 480
    |||||
Db 430 CTGGGTTCTCTGCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 489
Oy 481 ATTGCTGGTATCTGGGACCTTCAACATTTGAAGGAGTGAAGCTTCAACATTTGATC 540
    |||||
Db 490 ATTGCTGGTATCTGGGACCTTCAACATTTGAAGGAGTGAAGCTTCAACATTTGATC 549
Oy 541 ATCATTTGGCATCTGTGTACGTGATCCAGACGAGAGACTGCAAGATCAAGCATCA 600
    |||||
Db 550 ATCATTTGGCATCTGTGTACGTGATCCAGACGAGAGACTGCAAGATCAAGCATCA 609
Oy 601 CGAGTCTTCTCATACACGCTCTTGAAGTATCTTGTGCTACATCTGCTATATGATT 660
    |||||
Db 610 CGAGTCTTCTCATACACGCTCTTGAAGTATCTTGTGCTACATCTGCTATATGATT 669
Oy 661 CTGGGAGCTTCTCCCGGCTGGGCTGAGTTTGGGAAGGCTCTCTCACTCTCTCTC 720
    |||||
Db 670 CTGGGAGCTTCTCCCGGCTGGGCTGAGTTTGGGAAGGCTCTCTCACTCTCTCTC 729
Oy 721 TTTCCAGTGTGTGCTTGTGCTGAGTGAAGATTAACGACTCTCTTCAAAATAC 780
    |||||
Db 730 TTTCCAGTGTGTGCTTGTGCTGAGTGAAGATTAACGACTCTCTTCAAAATAC 789
Oy 781 ATGCACAAAAAGTACCAGACAGCAAAACCGAGGAATTTATATAGACAGAGGGTAC 840
    |||||
Db 790 ATGCACAAAAAGTACCAGACAGCAAAACCGAGGAATTTATATAGAGACAGAGGGTAC 849

```

OY	841	CACCTTAAGGGCATTTGGAGTGGAGGAAATGTAATTCATTCCTAGTGGGAAC	900
OY	841	CACCTTAAGGGCATTTGGAGTGGAGGAAATGTAATTCATTCCTAGTGGGAAC	900
Db	850	CACCTTAAGGGCATTTGGAGTGGAGGAAATGTAATTCATTCCTAGTGGGAAC	909
OY	901	CTGTGTCCTCGGAAGGGAAGGAAGTGGATGCCCGAGAGATGATCCGGATTCTC	960
Db	910	CTGGTGCCCTCGGAAGGGAAGGAAGTGGATGCCCGAGAGATGATCCGGATTCTC	969
OY	961	AAGGATCTGAAGCAAAAAACCCAGAGAGAGACTTGAATCAGCTGGTGGAGTGGCAAT	1020
Db	970	AAGGATCTGAAGCAAAAAACCCAGAGAGAGACTTGAATCAGCTGGTGGAGTGGCAAT	1023
OY	1021	TACTATGCTCTTTCCCAACGAAGAGCGGGGCTTCACCTGATTCGAAGCACTGCT	1080
Db	1030	TACTATGCTCTTTCCCAACGAAGAGCGGGGCTTCACCTGATTCGAAGCACTGCT	1089
OY	1081	ATGATGACTGGTGGAGGCAATATCTCTGAAGAAACATGCAAGCAAGCAAGAGGCGC	1144
Db	1090	ATGATGACTGGTGGAGGCAATATCTCTGAAGAAACATGCAAGCAAGCAAGAGGCGC	1144
OY	1141	TCGACGATGAGCGAGGTGCACACCGATGAGCTTGAGAGACTTTATTTCCAAAGTCTTCTT	1200
Db	1150	TCGACGATGAGCGAGGTGCACACCGATGAGCTTGAGAGACTTTATTTCCAAAGTCTTCTT	1209
OY	1201	GACCCATTTCTTCCAGTGGCTGGAAATGTTGGGGCTGTACTCTCGACAGTGGGAGG	1260
Db	1210	GACCCATTTCTTCCAGTGGCTGGAAATGTTGGGGCTGTACTCTCGACAGTGGGAGG	1266
OY	1261	AAAGGGGAGACATGTCAAAAGACCATGATGTGACTACAAAACAGAGAGTGGTCTGCC	1320
Db	1270	AAAGGGGAGACATGTCAAAAGACCATGATGTGACTACAAAACAGAGAGTGGTCTGCC	1322
OY	1331	AATGCAAGGGGCTGACTATGATTCACAGAGGCAAGGTGGTCTGAAGCCAGAGAGAC	1380
Db	1330	AATGCAAGGGGCTGACTATGATTCACAGAGGCAAGGTGGTCTGAAGCCAGAGAGAC	1389
OY	1381	CAGAAAGGATCTCTCGAGGGGCAATTAATGATGAGACATTTTGAGAGAGATGAACACTTC	1444
Db	1390	CAGAAAGGATCTCTCGAGGGGCAATTAATGATGAGACATTTTGAGAGAGATGAACACTTC	1445
OY	1441	TTTGTAAAGTGAACCAATGTCCGATAGAGAGAGACAGCAGAGAGAGGAGTGGCTCCA	1500
Db	1450	TTTGTAAAGTGAACCAATGTCCGATAGAGAGAGACAGCAGAGAGAGGAGTGGCTCCA	1509
OY	1501	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAAGCCTCCCTTGTGTGGCACA	1560
Db	1510	GCAATATTCAACAGTCTTCCCTTGCTCGGGCTGTCCTAAGCCTCCCTTGTGTGGCACA	1569
OY	1561	GTTACCACTCTGGATGATGACATGCAATGCAAGGATCTTCACTTTGAATGTATCTATCAT	1620
Db	1570	GTTACCACTCTGGATGATGACATGCAATGCAAGGATCTTCACTTTGAATGTATCTATCAT	1623
OY	1621	GTCAGTGAAGTATTTGGTGTATTATGAGAGGTCTCGGACATCAGGTGCCGGGGT	1680
Db	1630	GTCAGTGAAGTATTTGGTGTATTATGAGAGGTCTCGGACATCAGGTGCCGGGGT	1689
OY	1681	ACAGTCAATCGTCCCTTTAGAGACATGAAGGAGCAAGCAAGGTTGGCGTAGAGACTTT	1740
Db	1690	ACAGTCAATCGTCCCTTTAGAGACATGAAGGAGCAAGCAAGGTTGGCGTAGAGACTTT	1744
OY	1741	GAAAGCAATTTGGGGAGTTGGAAATTCAGAAATGATGAAGCAACTGTGAAGGAT	1800
Db	1750	GAAAGCAATTTGGGGAGTTGGAAATTCAGAAATGATGAAGCAACTGTGAAGGAT	1809
OY	1801	AAAAATAGTATGATGAGGAGAAATCGAAAGGCAAGAAATTTCTCACTTGGCTGGTGA	1860
Db	1810	AAAAATAGTATGATGAGGAGAAATCGAAAGGCAAGAAATTTCTCACTTGGCTGGTGA	1869
OY	1861	CCGAATATGATGGAACGTGTGAATATCAGATGTACAGACAGGAAGCTGCTATGGAAGA	1920
Db	1870	CCGAATATGATGGAACGTGTGAATATCAGATGTACAGACAGGAAGCTGCTATGGAAGA	1922
OY	1921	GAGAGGCCAAGAGATAGCAAGATGGGGAACCAAGTATTTGGGTGAACCCCAACTA	1980

Db	1930	GAGGAGGCCAGAGGATAGCAGAGTGGGAAAGCCAGTATTGGGTGAAACACCCCAACTG	1989
Qy	1981	GAAGTCATCATTTGAAGAGTCCATGATGATTCAAAGACTACGGTGGACAACTGATCAAGAG	2040
Db	1990	GAAGTCATCATTTGAAGAGTCCATGATGATTCAAAGACTACGGTGGACAACTGATCAAGAG	2049
Qy	2041	ACAAACCTGGCCCTTGGTTGTGGGGACCACTTCCTGGAGGAGACCACTTCATGAGAGGCCATTC	2100
Db	2050	ACAAACCTGGCCCTTGGTTGTGGGGACCACTTCCTGGAGGAGACCACTTCATGAGAGGCCATTC	2109
Qy	2101	ACCGTCAGTGCAGCAGGGGATGAGATGAGATGAAATCCGGGAGAGAGAGCGTCGCCCTCC	2160
Db	2110	ACCGTCAGTGCAGCAGGGGATGAGATGAGATGAAATCCGGGAGAGAGAGCGTCGCCCTCC	2169
Qy	2161	TGCTTTGACTACGTATGCATGCATCTCTGACTGTCTTCTGGAAAGTGCCTGTTGCCGTGTG	2220
Db	2170	TGCTTTGACTACGTATGCATGCATCTCTGACTGTCTTCTGGAAAGTGCCTGTTGCCGTGTG	2229
Qy	2221	CCCCCCACAGAGTACTGCGCACGCGCTGGGCCCTTCCGCCCTTCATCCTCATCTATTGGC	2280
Db	2230	CCCCCCACAGAGTACTGCGCACGCGCTGGGCCCTTCCGCCCTTCATCCTCATCTATTGGC	2289
Qy	2281	ATGCTCACCGCCATCATTTGGGGACCTGGCCCTGCACCTTTCGCGCTGCACCATTTGATCAAA	2340
Db	2290	ATGCTCACCGCCATCATTTGGGGACCTGGCCCTGCACCTTTCGCGCTGCACCATTTGATCAAA	2349
Qy	2341	GATTGAGTCACAGCTGTTGTGTTTCTGTGGCAATTTGGCACCTCTGTCCAGATACGTTTGCC	2400
Db	2350	GATTGAGTCACAGCTGTTGTGTTTCTGTGGCAATTTGGCACCTCTGTCCAGATACGTTTGCC	2409
Qy	2401	AGCAAGCTGCGGCCCTCCAGAGTATATGAGACGGCTCCATTTGGAGAGGTGACGGG	2460
Db	2410	AGCAAGCTGCGGCCCTCCAGAGTATATGAGACGGCTCCATTTGGAGAGGTGACGGG	2469
Qy	2461	AGCAACGCCGTCATATGTCTTCTGCGGCATCGGCTCGGCTGGTCCGTGGCGGCATCTAC	2520
Db	2470	AGCAACGCCGTCATATGTCTTCTGCGGCATCGGCTCGGCTGGTCCGTGGCGGCATCTAC	2529
Qy	2521	TGGGCTGTGCAGGAGCAGAGAGTTCCACGTTGTGCGCGGCACACTGGCCTTCTCGCTCAC	2580
Db	2530	TGGGCTGTGCAGGAGCAGAGAGTTCCACGTTGTGCGCGGCACACTGGCCTTCTCGCTCAC	2589
Qy	2581	CTCTTCACCATCTTGTGCATTTGTCTGCAATCAGCGGTCTTGTACCGAAAGCGGCGGCAC	2640
Db	2590	CTCTTCACCATCTTGTGCATTTGTCTGCAATCAGCGGTCTTGTACCGAAAGCGGCGGCAC	2649
Qy	2641	CTGGGAGGGAGACTGTGTGGCCCCCGGTGGATGTGCAGAGCTGCACCAACATAGGCTCTTTGTG	2700
Db	2650	CTGGGAGGGAGACTGTGTGGCCCCCGGTGGATGTGCAGAGCTGCACCAACATAGGCTCTTTGTG	2709
Qy	2701	AGCCTGTGGCTCTCTACATACCTCTTTGCCACACTAGAGGCCCTATTGCTACATCAAGGGG	2760
Db	2710	AGCCTGTGGCTCTCTACATACCTCTTTGCCACACTAGAGGCCCTATTGCTACATCAAGGGG	2769
Qy	2761	TTTCTAA 2766	
Db	2770	TTTCTAA 2775	

RESULT 3	
HSA304853	
LOCUS	
DEFINITION	HSA304853 2837 bp mRNA linear PRI 06-JUN-2001
	Homo sapiens mRNA for sodium/calcium exchanger, SCL8A3, alternative splicing form B (SCL8A3 gene).
ACCESSION	AJ304853
VERSION	AJ304853.1 GI:14330384
KEYWORDS	alternative splicing; Form B; SCL8A3 gene; SCL8A3 protein; Sodium/calcium exchanger.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2837)
AUTHORS Gabellini, N.
TITLE Characterization of the human SCL8A3 gene for solute carrier family 8, member 3 (sodium/calcium exchanger)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2837)
AUTHORS Bortoluzzi, S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and Department of Biological Chemistry, University of Padova, via G. Colombo 3, 35131 Padova, ITALY

FEATURES
source location/Ouallifiers
1..2837
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q24.1"
63..2837
/gene="SCL8A3"
63..2837
/gene="SCL8A3"
/function="sodium/calcium exchanger"
/note="alternative splice form B (exons 2, 4, 5, 9, 10, 11, 12)"
/codon_start=1
/product="sodium/calcium exchanger SCL8A3"
/protein_id="CAC40985.1"
/db_xref="GI:14330385"
/translation="MAMLRQLPLTSAFLHGLVTFVLNLGLRAEAGSGDVPSTGON NESCSGSSDCKEGLVLPYVNPENSLGDKLARVLYVVALYMLGLSIIDRMASI EVITSOBEVYIKKPNGETSTTTRVNNETVSNLTLMALGSABEILSLTEVGCHP IAGDLGSTIVGSAFNMFLIIGICVYVDPGETRKIKHLRFETITAMSTFAVIMLY MILLAVSPGVVQVMEGLTLTFEPVVCYLLANVADKRLFYTMKKRTKDBHRHITTE TEGDHPFGIEDGKMANSHFLDGNLVPLEGKVEDSRKEMIRILDKQKHPEVDLQ LVEHANYALSHOOKSRAFYRIQATRMATGAGNLKRNAAQAKASMSVHDEDE DFLSKVFEDPCSYGLENCAVILTVVRKGGDMKTMVVDYKTEGSGANAGADEFE GTVVLKGETOKESVGLIIDDIFEDEHFEVRLSNRIIEEOPEEGMPAIFNSLPL PRAVLASPVAVTVIIDDHAGITFPECDITHVESIGVMVVKRLRTSGAGCATVIVP RTVBSGTAAGSGDEDEPTVYGELEFKNDETIVKTRIKYIDEEYEIQENFTIAGPKKM BRGISALLSLSPDKLTWEEBARKIAEKGKVLDEHPKLEVIIESEYEKTVKLIK KTNLALVGHSHWMDQFMEALITVSAAGDEDESGERLPSCFDYVHMFLEKRVLE ACVPPEYCHGMACFAVSILITGLMTAIIIGDLASHFCTTIGLKSVAIVAVVAGTSY PDPEFASKAALIDVYADASIGNVTSNANVNFILGILAMSAALYMLAOGGEFVNSG TLASFVLTFTIFAFVCIISVILYRRRPHLGSGLGPRCKLATITWLFVSLMILYILFNT LEACYIKGF"

BASE COUNT 668 a 697 c 779 g 693 t

RIGIN

Query Match 99.0% Score 2737.4; DB 9; Length 2837;
Best Local similarity 99.5% Pred. No. 0;
Matches 2760; Conservative 0; Mismatches 6; Indels 9; Gaps 1;

QY 1 ATGGCGTGTAAAGGTTTCAGACCTCTACCTCTGCTTCCTCCATTTTGGCGTGTACC 60
DB 63 ATGGCGTGTAAAGGTTTCAGACCTCTACCTCTGCTTCCTCCATTTTGGCGTGTACC 122

QY 61 TTTGGCTCTTCTCAATAGTGTCTTGACAGAGAGCTGTGCTCAGGGACCTGCCAAC 120
DB 123 TTTGGCTCTTCTCAATAGTGTCTTGACAGAGAGCTGTGCTCAGGGACCTGCCAAC 182

QY 121 ACAGGGCAGAACATAGTCTGTTCAGAGGTCATCGAGCTGCAAGAGGGTGTCAATCG 180
DB 183 ACAGGGCAGAACATAGTCTGTTCAGAGGTCATCGAGCTGCAAGAGGGTGTCAATCG 242

QY 181 CCAATCTGTATACCCGAGAACCTTCCCTTGGGACAAGATTGCCAGGGTCAATGTCTAT 240
DB 243 CCAATCTGTATACCCGAGAACCTTCCCTTGGGACAAGATTGCCAGGGTCAATGTCTAT 302

QY 241 TTTGGGCGCTGATATATATGTCTTGGGGTGTCCATCATTCGTGACCGCTTCATGCA 300
DB 303 TTTGGGCGCTGATATATATGTCTTGGGGTGTCCATCATTCGTGACCGCTTCATGCA 362

QY 301 TCTATTGAAGTCATCAGCTCTCAAGAGAGGAGTGACAAATTAAAGAACCCCAATGAGAA 360

DB 363 TCTATTGAAGTCATCAGCTCTCAAGAGAGGAGTGACAAATTAAAGAACCCCAATGAGAA 422
QY 361 ACCAGCACACACCAATATTCGGGTCTGGAATGAACCTGTCTCCACCTGATGGCC 420
DB 423 ACCAGCACACACCAATATTCGGGTCTGGAATGAACCTGTCTCCACCTGATGGCC 482
QY 421 CTGGGTTCTCTGCTGCTGAGATGATCTCCCTCTTAAATTAAGAGTGTGGTATGGGTT 480
DB 483 CTGGGTTCTCTGCTGCTGAGATGATCTCCCTCTTAAATTAAGAGTGTGGTATGGGTT 542
QY 481 ATTGTGTGATCTGGGACCTTCTACATTTGAGGAGGTGACGCTTCAACATGTTTCATC 540
DB 543 ATTGTGTGATCTGGGACCTTCTACATTTGAGGAGGTGACGCTTCAACATGTTTCATC 602
QY 541 ATCATTTGGCATCTGTGTCTACGTATCCAGACGAGAGACTCGCAAGATCAAGCATCTA 600
DB 603 ATCATTTGGCATCTGTGTCTACGTATCCAGACGAGAGACTCGCAAGATCAAGCATCTA 662
QY 601 CGAGTCTTCTTCATACCGCTGCTTGGAGTATCTTGGCTACATCTGGCTATATGANT 660
DB 663 CGAGTCTTCTTCATACCGCTGCTTGGAGTATCTTGGCTACATCTGGCTATATGANT 722
QY 661 CTGGAGTCTTCTCCCTGCTGTGGTCCAGGTTTGGAAAGGCTCTCACCTCTTCTTC 720
DB 723 CTGGAGTCTTCTCCCTGCTGTGGTCCAGGTTTGGAAAGGCTCTCACCTCTTCTTC 782
QY 721 TTTCCAGTGTGTGCTCTTCTGCGCTTGGGTGGAGATTAACGACTCTCTTCAAAATAC 780
DB 783 TTTCCAGTGTGTGCTCTTCTGCGCTTGGGTGGAGATTAACGACTCTCTTCAAAATAC 842
QY 781 ATGCACAAAAGTACCAGACAGACAAACCCAGAGAAATTATCATATGAGACAGAGGTGAC 840
DB 843 ATGCACAAAAGTACCAGACAGACAAACCCAGAGAAATTATCATATGAGACAGAGGTGAC 902
QY 841 CACCTTAAGGCGATGAGATGATGGGAAAGATGAATTCCTATTTCTATAGTGGAAAC 900
DB 903 CACCTTAAGGCGATGAGATGATGGGAAAGATGAATTCCTATTTCTATAGTGGAAAC 962
QY 901 CTGTGTCCCTCTGGAAAGGAGAGTGTGATGATGTCCTCCAGAGAGATGATCCGATTC 960
DB 963 CTGTGTCCCTCTGGAAAGGAGAGTGTGATGATGTCCTCCAGAGAGATGATCCGATTC 1022
QY 961 AAGGATCTGAACCAAAACACCCAGAGAAAGACTTATGATCAGCTGTGAGATGGCCAT 1020
DB 1023 AAGGATCTGAACCAAAACACCCAGAGAAAGACTTATGATCAGCTGTGAGATGGCCAT 1082
QY 1021 TACTATGCTCTTCCACCAACAGAAAGCCGCTTCTACCGTATCCAAACCACTGCT 1080
DB 1083 TACTATGCTCTTCCACCAACAGAAAGCCGCTTCTACCGTATCCAAACCACTGCT 1142
QY 1081 ATGATGACTGTGTGACGCAATATCTGTAAGAAACATGACGACGAACCAAGAGAGCC 1140
DB 1143 ATGATGACTGTGTGACGCAATATCTGTAAGAAACATGACGACGAACCAAGAGAGCC 1202
QY 1141 TCCAGCATGAGGAGGTGACACACCATGAGCTGTGAGAGCTTATTTCCAAAGTCTTCTTT 1200
DB 1203 TCCAGCATGAGGAGGTGACACACCATGAGCTGTGAGAGCTTATTTCCAAAGTCTTCTTT 1262
QY 1201 GACCATGCTTCTTACAGTGCCTGGAGAACTGTGGGGCTGTACTCTCTGACATGTGAG 1260
DB 1263 GACCATGCTTCTTACAGTGCCTGGAGAACTGTGGGGCTGTACTCTCTGACATGTGAG 1322
QY 1261 AAAGGGGAGACATGTCAAAAGACATGTATGTGACACTCAAAACAGAGAGTGTCTGCG 1320
DB 1323 AAAGGGGAGACATGTCAAAAGACATGTATGTGACACTCAAAACAGAGAGTGTCTGCG 1382
QY 1321 AATGAGGGGCTGACTATGAGTTCAAGAGGCGACAGGCTGTCTAAGCAGAGAGAGAC 1380
DB 1383 AATGAGGGGCTGACTATGAGTTCAAGAGGCGACAGGCTGTCTAAGCAGAGAGAGAC 1442
QY 1381 CAGAAGAGTCTCCGTGGGCAATAATGATGACGACATTTTGAAGAGATGAACACTTC 1440

Db	1443	CAGAAAGGAGTTCTCCGGTGGGCAATTAATTGATGACGACATTTTGTGAGSAGATGAACACTTC	1502
Qy	1441	TTTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGACACCAGAGAGGGATGCTCTCA	1500
Db	1503	TTTTGTAAAGTTGAGCAATGTCCGCATAGAGGAGACACCAGAGAGGGATGCTCTCA	1562
Qy	1501	GCATATTCAACACACTCTCCCTTGCCGGGGGTGTCTGACCTCCCTCTGTGTGGCCACA	1566
Db	1563	GCATATTCAACACACTCTCCCTTGCCGGGGGTGTCTGACCTCCCTCTGTGTGGCCACA	1622
Qy	1561	GTATACACTTTGGATGATGACCAATGCAGGCATCTTCACTTTGAAATGATACATAT	1620
Db	1623	GTATACACTTTGGATGATGACCAATGCAGGCATCTTCACTTTGAAATGATACATAT	1682
Qy	1621	GTCACTGAGACTATTGGTATTATGAGCTCAAGTTCTCGGCATCAAGTCCCGGGGT	1680
Db	1683	GTCACTGAGACTATTGGTATTATGAGCTCAAGTTCTCGGCATCAAGTCCCGGGGT	1742
Qy	1681	ACAGTCACTCTCCCTTTAGSACATGTAAGAGGACGCCAAGGGTGTGGGTAGACATTT	1740
Db	1743	ACAGTCACTCTCCCTTTAGSACATGTAAGAGGACGCCAAGGGTGTGGGTAGACATTT	1802
Qy	1741	GAAGACACATATGGGGAGTTGGAAATTCAAATGATGAACATGTGAAACCATTAAGGGTT	1800
Db	1803	GAGACACATATGGGGAGTTGGAAATTCAAATGATGAACATGTGAAACCATTAAGGGTT	1862
Qy	1801	AAAATAGTAGATGAGGAGGAATACGAAGGCAAGAAATTTCTCATTTGCCCTTGSTAA	1860
Db	1863	AAAATAGTAGATGAGGAGGAATACGAAGGCAAGAAATTTCTCATTTGCCCTTGSTAA	1922
Qy	1861	CCGAATGTGATGGAAGCTGGAAATTCATGATGT-----GACGACAGGAAGCTGACT	1911
Db	1923	CCGAATGTGATGGAAGCTGGAAATTCATGACGCTCTGTATTCTCCAGACAGGAAGCTGACT	1982
Qy	1912	ATGGAAGAAGGAGGGCCCAAGAGGATAGCAGAGATGGGAAGCCAGATTTGGGTGAACAC	1971
Db	1983	ATGGAAGAAGGAGGGCCCAAGAGGATAGCAGAGATGGGAAGCCAGATTTGGGTGAACAC	2042
Qy	1972	CCCAAACTAGAAGTCATATTGAAGATCCTTATGATTAAGACTACGCTGAGCAAACTG	2031
Db	2043	CCCAAACTAGAAGTCATATTGAAGATCCTTATGATTAAGACTACGCTGAGCAAACTG	2102
Qy	2032	ATCAAGAAGACAAACCTGTGGCTTGTGTGGGACCCATTTCTGGAAGGACCAATTCATG	2091
Db	2103	ATCAAGAAGACAAACCTGTGGCTTGTGTGGGACCCATTTCTGGAAGGACCAATTCATG	2162
Qy	2092	GAGGCATACACCGTCAGTCAGCAGCAGGGGATGAGATGAGAGATGAATCCGGGGAGGAGG	2151
Db	2163	GAGGCATACACCGTCAGTCAGCAGCAGGGGATGAGATGAGAGATGAATCCGGGGAGGAGG	2222
Qy	2152	CTGCCCTCTGCTTTGACTACGTCAATGCACTTCTGACTGTCTTGTGAAAGGTGCTGTTT	2211
Db	2223	CTGCCCTCTGCTTTGACTACGTCAATGCACTTCTGACTGTCTTGTGAAAGGTGCTGTTT	2282
Qy	2212	GCCTGTGTGCCCCCACAAGATACGTGCACAGGCTGGGCTGCTTGCGCTCTCAATCCTC	2271
Db	2283	GCCTGTGTGCCCCCACAAGATACGTGCACAGGCTGGGCTGCTTGCGCTCTCAATCCTC	2342
Qy	2272	ATCAATGTGCATGTCAACGGCACAATTTGGGAGACCTGGCTCCCACTTGTGGCTGACACTT	2331
Db	2343	ATCAATGTGCATGTCAACGGCACAATTTGGGAGACCTGGCTCCCACTTGTGGCTGACACTT	2402
Qy	2332	GGTCTCAAAAGTATTAGTCACAGCTGTGTGTTTCTGTGGCAATTTGGACACTCTGTCCCAAT	2391
Db	2403	GGTCTCAAAAGTATTAGTCACAGCTGTGTGTTTCTGTGGCAATTTGGACACTCTGTCCCAAT	2462
Qy	2392	ACGTTTGGCAGCAAAAGCTGTGCTGCCTTCAGAGATGTATTATGACAGACGCTTCATTGGCAAC	2451
Db	2463	ACGTTTGGCAGCAAAAGCTGTGCTGCCTTCAGAGATGTATTATGACAGACGCTTCATTGGCAAC	2522
Qy	2452	GTGACGGGACAGCAACGCCGTCATATGTCTTCGTGTGGCATGTGGCTGTGCTGTGCTGGCC	2511
Db	2523	GTGACGGGACAGCAACGCCGTCATATGTCTTCGTGTGGCATGTGGCTGTGCTGTGCTGGCC	2582

QY	2512	GCATCTACTGGGCTCTGAGGAGACAGAGATTCACAGTGTGGCGGACACATGGGCTTC	2571		
Db	2583	GGCATCTACTGGGCTCTGAGGAGACAGAGATTCACAGTGTGGCGGACACATGGGCTTC	2642		
QY	2572	TCCGTCACCCCTCTGCACATCTTTGGATTGTGCTGCATCAGGCTGCTCTTGTACCGAAG	2631		
Db	2643	TCCGTCACCCCTCTGCACATCTTTGGATTGTGCTGCATCAGGCTGCTCTTGTACCGAAG	2702		
QY	2632	CGGCGCACCTTGGAGGGAGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACACATG	2691		
Db	2703	CGGCGCACCTTGGAGGGAGAGCTTGGTGGCCCCCGTGGCTGCAAGCTCGCCACACATG	2762		
QY	2692	CTCTTTGTAGGCTGTGGCTTCCTTCATACATCTTTGGCACACTAGAGGCTATTGGCTAC	2751		
Db	2763	CTCTTTGTAGGCTGTGGCTTCCTTCATACATCTTTGGCACACTAGAGGCTATTGGCTAC	2822		
QY	2752	ATCAAGGGGTTCTAA 2766			
Db	2823	ATCAAGGGGTTCTAA 2837			
RESULT 4	AX299471	2781 bp	DNA	linear	PAT 26-NOV-2001
LOCUS	AX299471				
DEFINITION	Sequence 1 from Patent WO0183744.				
ACCESSION	AX299471				
VERSION	AX299471.1	GI:17129228			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Wilm, C.				
TITLE	Sodium-calcium exchanger protein				
JOURNAL	Patent: WO 0183744-A 1 08-NOV-2001;				
FEATURES	MERCK PATENT GmbH (DE)				
Source	Location/Qualifiers				
	1..2781				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	1..>2781				
	/note="unnamed protein product"				
	/codon_start=1				
	/protein_id="CAD12716.1"				
	/db_xref="GI:17129228"				
	/translation="MAWLRLQPLTSAFLHFGLVTFVFLFLNGLRAEGSGDVPSTGON				
	NESGSSDCKEGVLPPIWYPENPSLGDRIARIVYFVALIYMLGSAIIADREMAS				
	IVITQERETVTKRPNGETSTTTIKVNNETSNLTLMLAGSABEILLSEVGHGHS				
	IAGDGPSTIVGSAFNMETIIIGICVYIIPGERTKIHLEVPFTAMSLFEAYIMLP				
	MLVAEFSQVQVMEGLITLFFPPYCVLAWVAADKRLILEYVMKRYPTDKHRIIIE				
	TEGHPKRIENDKKMNSHPLDGNLVPLEGVEVDESREMRIRLKLQKRPENDLDC				
	LVEANVYALSHQOKSRAFYRIQATRMNTGAGNLIKRAAQAOKASSMSVHTDERP				
	DTIVKPEFDPQSYOLENGCAVLITLVKRGDMSTMYVDKTEGDSANAGADEFEH				
	GVTVLKPGETQKEFSVGIIDDDIEEDDEHFEFVRLSNVRIIEEOPEEGMPAIFNSLP				
	PRAVLASPCVATVTIILDDHAGIFPEEDCTIHVSRSIGVMEKVLRTSGANGTVIPE				
	RTVETAKGGEDEEDPYGLEEFKNDEVKTIIRKYIIDEFEYQENFTILGPKKMA				
	ERGISGVAFKFDVTDRLKLTMBEERKRIAEKGRVYLGHKRLVYIIESTYFKTTVDK				
	LIKITNLVLVGTGHWMDQFMEALITVMSAAGDEDESECEPSCDFVHFLVTFVAK				
	LVFACVPTVEYCHGMACPAVSILITGLMTALIGDASHFGCTIGLKDSPAIVAVFAR				
	TSVDTEFSKAAALODYVADASIGNVTSNANVNFELGILAMSVAAIYMALQCEFHV				
	SAGTLAEVSLTFTTTFAPVCIISVLLYRRPHLGELGGRCKLATVTMLFVSLMLITL				
	FATLEAYKINGF"				
BASE COUNT	658 a	678 c	765 g	860 t	
ORIGIN					
Query Match	98.8%;	Score 2733.4;	DB 6;	Length 2781;	
Best Local Similarity	99.3%;	Pred. No. 0;			
Matches 2762;	Conservative	0;	Mismatches	1;	Indels 18; Gaps 1;
QY	1	ATGGCGTGGTTAAGCTTGCAGGCTCTACACCTTCGCTTCACATTTGGCGTGGTTACG	60		

D	b	1	ATGCGCTGGTTAAAGGTGGACGCTCTACACCTCGCTCCCTCCATCTTTGGGCTGGTTACC	60
O	y	61	TTTGTGCTCTTCCTGAAATGGTCTTTCGACGAGAGCGCTGTTGGCTCAGGGGACGTGCCAAGC	120
D	b	61	TTTGTGCTCTTCCTGAAATGGTCTTTCGACGAGAGCGCTGTTGGCTCAGGGGACGTGCCAAGC	120
O	y	121	ACAGGGCAGAAACATAGTCTCTTTACAGGTCATCGGACTGCAGAGAGGTGTATCCTG	180
D	b	121	ACAGGGCAGAAACATAGTCTCTTTACAGGTCATCGGACTGCAGAGAGGTGTATCCTG	180
O	y	181	CCATCTGAGTACCCGGGGAACCCCTTCCCTTGGGGACAAGATTTGCCAGGGTCAATGTCTAT	240
D	b	181	CCATCTGAGTACCCGGGGAACCCCTTCCCTTGGGGACAAGATTTGCCAGGGTCAATGTCTAT	240
O	y	241	TTTGTGGCCCTGATATATACATGTCTCTTGGGGGTGTCCATCATTTGCTGACCGCTTCATGGCA	300
D	b	241	TTTGTGGCCCTGATATATACATGTCTCTTGGGGGTGTCCATCATTTGCTGACCGCTTCATGGCA	300
O	y	301	TCCTATTGAAGTCATACCTCTTCAAGAGAGGAGGTGACATTTAGAAACCAATGAGAAA	360
D	b	301	TCCTATTGAAGTCATACCTCTTCAAGAGAGGAGGTGACATTTAGAAACCAATGAGAAA	360
O	y	361	ACGAGCAACACACTATTTGGGGCTGGAGTTGAACGTGTCCAACTGACCTTAATGGCC	420
D	b	361	ACGAGCAACACACTATTTGGGGCTGGAGTTGAACGTGTCCAACTGACCTTAATGGCC	420
O	y	421	CTGGGTTCTCTGCTCCTGAGATACCTCTCTCTTTAATTGAGAGTGTGGTGCATGGGTTTC	480
D	b	421	CTGGGTTCTCTGCTCCTGAGATACCTCTCTCTTTAATTGAGAGTGTGGTGCATGGGTTTC	480
O	y	481	ATTCTGTGTATCTGGGACCTTCTACCAATTGTAGGAGTGCAGCCTTGACATGTTCATC	540
D	b	481	ATTCTGTGTATCTGGGACCTTCTACCAATTGTAGGAGTGCAGCCTTGACATGTTCATC	540
O	y	541	ATTCATTGGCACTGTGTCTGTACGTGATCCCAAGAGAGAGTCCGAAATCAACATCACTA	600
D	b	541	ATTCATTGGCACTGTGTCTGTACGTGATCCCAAGAGAGAGTCCGAAATCAACATCACTA	600
O	y	601	CGAATCTTTCATCAACACCGCTGCTGTGGAGTATCTTGGCCATCATGTGGCTCTAATGATT	660
D	b	601	CGAATCTTTCATCAACACCGCTGCTGTGGAGTATCTTGGCCATCATGTGGCTCTAATGATT	660
O	y	661	CTGGCAGTCTTCTCCCTGCTGTGTGTCCAGGTTTGGGAAGGCTCTCACTCTCTTCTTC	720
D	b	661	CTGGCAGTCTTCTCCCTGCTGTGTGTCCAGGTTTGGGAAGGCTCTCACTCTCTTCTTC	720
O	y	721	TTTTCAGTGTGTGTCTTCTTGGGCTGGGTGGCGAGATTAACGACCTCTCTTCTACAAATAC	780
D	b	721	TTTTCAGTGTGTGTCTTCTTGGGCTGGGTGGCGAGATTAACGACCTCTCTTCTACAAATAC	780
O	y	781	ATGCACAAAAAGTACCCGACAGACAAACACCGAGAAATTATATGAGACAGAGGGTAC	840
D	b	781	ATGCACAAAAAGTACCCGACAGACAAACACCGAGAAATTATATGAGACAGAGGGTAC	840
O	y	841	CACCCCTAAGGGCATTTGAGATGATGGGAAATGATGAATTTCCATTTTCTAGATGGGAC	900
D	b	841	CACCCCTAAGGGCATTTGAGATGATGGGAAATGATGAATTTCCATTTTCTAGATGGGAC	900
O	y	901	CTGTGTGCCCTCGGAAGGGAAGGATGTAGTGTCCCGGAGAGATATCTCGGATTTCTC	960
D	b	901	CTGTGTGCCCTCGGAAGGGAAGGATGTAGTGTCCCGGAGAGATATCTCGGATTTCTC	960
O	y	961	AAGGATCTGAAGCAAAAAACCCAGAGAAAGACTTATGATCACTGTGTGAGATGGCCAAAT	1020
D	b	961	AAGGATCTGAAGCAAAAAACCCAGAGAAAGACTTATGATCACTGTGTGAGATGGCCAAAT	1020
O	y	1021	TACTATGCTCTTTCGCCACCAACAGAGAGAGCGCGCTTCTTACCTGTATCAAGCCACTGT	1080
D	b	1021	TACTATGCTCTTTCGCCACCAACAGAGAGAGCGCGCTTCTTACCTGTGTATCAAGCCACTGT	1080
O	y	1081	ATGATGACTGTGTGAGGCAATATCTCTGAAGAAACATGACGACGAACAGCAAGAGGCC	1140
D	b	1081	ATGATGACTGTGTGAGGCAATATCTCTGAAGAAACATGACGACGAACAGCAAGAGGCC	1140

QY	1141	TCACGATGAGGAGAGTGCACACCGCATGAGCTTATTTCCAAAGTCTTCTTT	1200
Db	1141	TCACCATGAGGAGAGTGCACACCGCATGAGCTTATTTCCAAAGTCTTCTTT	1200
QY	1201	GACCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCCTCAACATGSGTGAG	1260
Db	1201	GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCTCACTGSGTGAG	1260
QY	1261	AAAGGGGAGACATGTCAAAGCATTGTATGTGACTACAAAACAGAGATGTTCTGCC	1320
Db	1261	AAAGGGGGAGACATGTCAAAGCATTGTATGTGGACTACAAAACAGAGATGTTCTGCC	1320
QY	1321	AATGCAGGGGCTGCATGTAGTTTCACAGAGGGCACGGGTGTTCTGAAGCAGAGAGACC	1380
Db	1321	AATGCAGGGGCTGCATGTAGTTTCACAGAGGGCACGGGTGTTCTGAAGCAGAGAGACC	1380
QY	1381	CAGAAAGGATTCCTCGTGGGCATTAATTGATGACGACATTTTGGAGAGATGAMACATTC	1440
Db	1381	CAGAAAGGATTCCTCGTGGGCATTAATTGATGACGACATTTTGGAGAGATGAMACATTC	1440
QY	1441	TTTGTAAAGTTAGCAATCTCCGCATTAAGAGAGACAGCCAGAGAGGATGTCCTCA	1500
Db	1441	TTTGTAAAGTTAGCAATCTCCGCATTAAGAGAGACAGCCAGAGAGGATGTCCTCA	1500
QY	1501	GCAATATTTCAACAGTCTTCCTTGGCTGGGCTGTCTAGCCTCCGCTTGTGTGGCACA	1560
Db	1501	GCAATATTTCAACAGTCTTCCTTGGCTGGGCTGTCTAGCCTCCGCTTGTGTGGCACA	1560
QY	1561	GTTTACCATTGGAATGATGATGACCATGACGAGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
Db	1561	GTTTACCATTGGAATGATGATGACCATGACGAGCATCTTCACTTTTGAATGTGATACTATTCAT	1620
QY	1621	GTCAGTGAAGATTAATGGTGTATATGAGAGTCAAGGTTCTGCGACATCAGTGCCTGGGGT	1680
Db	1621	GTCAGTGAAGATTAATGGTGTATATGAGAGTCAAGGTTCTGCGACATCAGTGCCTGGGGT	1680
QY	1681	ACAGTCATGTCCTCCCTTTAGACAGTAGAAGGGACAGCCAAAGGTTGGCGGTGAGGACTTT	1740
Db	1681	ACAGTCATGTCCTCCCTTTAGACAGTAGAAGGGACAGCCAAAGGTTGGCGGTGAGGACTTT	1740
QY	1741	GAAAGCACATATGGGGAGTTGGAATTCAMGATGTGATGAACATGTGTAACATTAAGGGTT	1800
Db	1741	GAAAGCACATATGGGGAGTTGGAATTCAMGATGTGATGAACATGTGTAACATTAAGGGTT	1800
QY	1801	AAATATAGTATGATGAGAGGAAATACGAAGAAGCAAGAAATTTCTTATTTGCCCTTGSTGA	1860
Db	1801	AAATATAGTATGATGAGAGGAAATACGAAGAAGCAAGAAATTTCTTATTTGCCCTTGSTGA	1860
QY	1861	CCGAAATGATGGAACGTGGAATATC-----AGATGTGACAGACAG	1902
Db	1861	CCGAAATGATGGAACGTGGAATATCAGGTGTGAAATTTTAAAGATGTGACACAG	1920
QY	1903	AAGCTGACTATGGAAGAAAGAGAGGCGCAAGAGATAGCAAGATGAGGAAAGCCAGATATG	1962
Db	1921	AAGCTGACTATGGAAGAAAGAGAGGCGCAAGAGATAGCAAGATGAGGAAAGCCAGATATG	1980
QY	1963	GGTGAACACCCCAACTAGAACTCATTTGAAGAGTCTTATGACTTCAAGACTACGGTG	2022
Db	1981	GGTGAACACCCCAACTAGAACTCATTTGAAGAGTCTTATGAGTTCAAAGACTACGGTG	2040
QY	2023	GACAAATCTATCAAGAAAGCAAACTCGGCTTGTTGTGGGAGACCATTTCTGAGAGGAC	2082
Db	2041	GACAAATCTATCAAGAAAGCAAACTCGGCTTGTTGTGGGAGACCATTTCTGAGAGGAC	2100
QY	2083	CAGTTCATGAGAGGCATCACGCTCAAGTGCAGCAGAGGGATGAGAGTGAAGATTAATCCGG	2142
Db	2101	CAGTTCATGAGAGGCATCACGCTCAAGTGCAGCAGAGGGATGAGAGTGAATTAATCCGG	2160
QY	2143	GAGGAGAGGCTCCCTCTGCTTTGACTACGTATGACATCTTCTGACTGTCTTCTGGAAG	2202
Db	2161	GAGGAGAGGCTCCCTCTGCTTTGACTACGTATGACATCTTCTGACTGTCTTCTGGAAG	2220

QY 2203 GTGCTGTTTGGCCGTGTGTGCCCCACAGAGTACTGCCACGGCTGGCCCTCTTCCGCGTC 2262
|||||
Db 2221 GTGCTGTTTGGCCGTGTGTGCCCCACAGAGTACTGCCACGGCTGGCCCTCTTCCGCGTC 2280
|||||
QY 2263 TCCATCTCTATCATTTGGCATGCTCACCAGCATATTGGGACCTGGCCTTGCACTTGGC 2222
|||||
Db 2281 TCCATCTCTATCATTTGGCATGCTCACCAGCATATTGGGACCTGGCCTTGCACTTGGC 2240
|||||
QY 2323 TGCACCATTTGGCTCAAAAGATTGATGATCAGTCACTGTTGTTTGGGGCATTTGGCACCTCT 2382
|||||
Db 2341 TGCACCATTTGGCTCAAAAGATTGATGATCAGTCACTGTTGTTTGGGGCATTTGGCACCTCT 2400
|||||
QY 2383 GTCCCAAGATACGTTTGGCCAGCAAAAGCTGCTCCCTCAGAGATGTATATGACAGAGCCCTCC 2442
|||||
Db 2401 GTCCCAAGATACGTTTGGCCAGCAAAAGCTGCTCCCTCAGAGATGTATATGACAGAGCCCTCC 2460
|||||
QY 2443 ATTGGCAAGCTGACGGGACAGCAAGCCGTAAATGCTCTCTGGGACATGGCCTTGCCCTGG 2502
|||||
Db 2461 ATTGGCAAGCTGACGGGACAGCAAGCCGTAAATGCTCTCTGGGACATGGCCTTGCCCTGG 2520
|||||
QY 2503 TCCGTGGCCGCGCATCTACTGCGCTGTGACAGGAGAGATTCCACGTTGCGCGCGGACACA 2562
|||||
Db 2521 TCCGTGGCCGCGCATCTACTGCGCTGTGACAGGAGAGATTCCACGTTGCGCGCGGACACA 2580
|||||
QY 2563 CTGGCCTTCTCGCTCAACCTCTTCCACATCTTTGCAATTTGTCATACAGCGTCTCTTG 2622
|||||
Db 2581 CTGGCCTTCTCGCTCAACCTCTTCCACATCTTTGCAATTTGTCATACAGCGTCTCTTG 2640
|||||
QY 2623 TACCGAAGGGGGCGGACCTGCGAGGGAGCTGTGGCCCGCGTGGCTCAAGCTCGCC 2682
|||||
Db 2641 TACCGAAGGGGGCGGACCTGCGAGGGAGCTGTGGCCCGCGTGGCTCAAGCTCGCC 2700
|||||
QY 2683 ACAACATGAGCTCTTTGTGAGACCTGTGGCTCTCTACATACTCTTTGCGACACATAGAGGCC 2742
|||||
Db 2701 ACAACATGAGCTCTTTGTGAGACCTGTGGCTCTCTACATACTCTTTGCGACACATAGAGGCC 2760
|||||
QY 2743 TATTGCTACATCAAGGGGTTTC 2763
|||||
Db 2761 TATTGCTACATCAAGGGGTTTC 2781
|||||

RESULT 5
HSA304852 2840 bp mRNA linear PRI 06-JUN-2001
LOCUS HSA304852
DEFINITION Homo sapiens mRNA for sodium/calcium exchanger SCL8A3, alternative
splice form A (SCL8A3 gene).
ACCESSION AJ304852.1 GI:14330382
VERSION AJ304852.1
KEYWORDS alternative splicing; form A; SCL8A3 gene; SCL8A3 protein;
Sodium/calcium exchanger.
URCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2840)
AUTHORS Gabelini, N.
TITLE Characterization of the human SCL8A3 gene for solute carrier family
8, member 3 (sodium/calcium exchanger)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2840)
AUTHORS Bortoluzzi, S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and
Department of Biological Chemistry, University of Padova, via G.
Colombo 3, 35131 PADOVA, ITALY

FEATURES
source
1..2840
Location/Qualifiers

gene
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q24.1"
63..2840
/gene="SCL8A3"

CDS
63..2840
/gene="SCL8A3"
/function="sodium/calcium exchanger"
/note="alternative splice form A, (exons 2, 3, 5, 9, 10,
11, 12)"
/codon_start=1
/product="sodium/calcium exchanger SCL8A3"
/protein_id="CAC40984.1"
/db_xref="GI:14330383"
/translation="MANLRLQPLTSLNLFHGLVTVPLFNGLRARAGSGDVPSTGON
NBSGSSDCKRGVILPIWYPERNSIDGLTAVIYFVALITMFLGVSLIARFNASI
EVIISQEREVITIKKPNGETSTTIRWNETSVNLTLMAIGSSAPBLLSLIECGHF
IAGDLGPTIVGSAAFNMFIIIGICVYIPDETRIKHLRVEFTIAMSISYITMY
MLIAVSPGVOWMEGLTLFFEPVCLLAWADRLEKLYKMKHKKRDKRGILIE
TEGDHPKGIEMDGKMNHSHFLDGNLVPELGRVDSRREMIIKLDKOKHDEKID
LYEMANYALSHOOKSRATRYOATRPMNGANIIKKHAEDAKKASSMSVYDPE
DITSKFFDPCSTQCLNCGAVALTVYRKGGMSTMYVDYITDEGSNAGADYETE
GTVLAKPGETQKESVGIIDDDIFEDEHFFVLRNSVRIEEOPEBGPALFNSLP
PRAVLASPCVATVTLIDDDHAGIFTEEDCTIHVSISIGVMEKVNRTSGARCTVLP
RIVEGTAKGGEDEPDTYGELEFKNDEYKTIHRYIDEALEYKKNYETEMKGRMV
DMSFOKALLSPDRKLTMEEBAKRIAEKGFVLGHPRLVLEYIESEYEFKTVKLI
KRTNLALVYGHSHMRDOPMEATTVSAAGDEDESGEERLPCSPVYMLFLVFKVL
PACVPEPEYCHRMACPANSITLITGHTALITGLASHFGCTTGLKSVYAVVVAAGTS
VPDTRASKAALQADVADASIGNVTSNAVNVLFIGLAMSVAAIYMALQGEHFVSA
GTLAFSVTLFTIFAEVCIISVLLYRRRPHLGELGPRCKLATWLFVSLMLYILFA
TLEAVCYIKGF"

BASE COUNT 668 a 700 c 775 g 697 t
ORIGIN
Query Match 96.1%; Score 2657.6; DB 9; Length 2840;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 2712; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

QY 1 ATGGCGGTGTTAAGTTGACGCTCACCTCGCTCCCTCCATTTGGGCGGTATACC 60
|||||
Db 63 ATGGCGGTGTTAAGTTGACGCTCACCTCGCTCCCTCCATTTGGGCGGTATACC 122
|||||
QY 61 TTTGTGCTCTTCTGATAGTGTCTTTCAGACAGAGCGTGTGGCTCAAGGGACGTGCCAAC 120
|||||
Db 123 TTTGTGCTCTTCTGATAGTGTCTTTCAGACAGAGCGTGTGGCTCAAGGGACGTGCCAAC 182
|||||
QY 121 ACAGGCGACAAATGATGCTCTTCAGGGTCATCGGACTGCAAGAGAGGGTGTCACTCTG 180
|||||
Db 183 ACAGGCGACAAATGATGCTCTTCAGGGTCATCGGACTGCAAGAGAGGGTGTCACTCTG 242
|||||
QY 181 CCATCTGGTACCCGGAGAACCTTCCCTTGGGAGACAAGTTGCCAGGGCATTTGTCAT 240
|||||
Db 243 CCATCTGGTACCCGGAGAACCTTCCCTTGGGAGACAAGTTGCCAGGGCATTTGTCAT 302
|||||
QY 241 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATCTTGCATGCCCTTCATGGCA 300
|||||
Db 303 TTTGTGGCCCTGATATACATGTTCTTGGGGTGTCCATCATCTTGCATGCCCTTCATGGCA 362
|||||
QY 301 TCTATTGAAGTCACTACCTCTCAAGAGAGGAGGTGACATTTAAGAAACCAATGAGAA 360
|||||
Db 363 TCTATTGAAGTCACTACCTCTCAAGAGAGGAGGTGACATTTAAGAAACCAATGAGAA 422
|||||
QY 361 ACCAGACAAACCTATTTGGGGCTGTGAATGAAGTGTCCCAACTGACCCCTTATGGCC 420
|||||
Db 423 ACCAGACAAACCTATTTGGGGCTGTGAATGAAGTGTCCCAACTGACCCCTTATGGCC 482
|||||
QY 421 CTGGGTTCTCTGCTCCTGAGATACCTCTCTTTAATTGAGGTGTGTGTCATGGGTTTC 480
|||||
Db 483 CTGGGTTCTCTGCTCCTGAGATACCTCTCTTTAATTGAGGTGTGTGTCATGGGTTTC 542
|||||
QY 481 ATTGCTGTGATCTGGGACCTTCTACCATTTTGGAGATGACACCTTCACATGTTTCATC 540
|||||
Db 543 ATTGCTGTGATCTGGGACCTTCTACCATTTTGGAGATGACACCTTCACATGTTTCATC 602
|||||
QY 541 ATCATTTGCGATCTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTTA 600
|||||
Db 603 ATCATTTGCGATCTGTCTACGTGATCCAGACGGAGAGACTCGCAAGATCAAGCATCTTA 662
|||||

601 CGAGTCTTCTTCATCAGCCGCTGTGGAGTATCTTGGCTACATGCTCTATATGAT 660
|||||
663 CGAGTCTTCTTCATCAGCCGCTGTGGAGTATCTTGGCTACATGCTCTATATGAT 722
Db
661 CTGGCAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGCCCTCTACTCTCTTTC 720
|||||
723 CTGGGAGTCTTCTCCCTGGTGTGGTCCAGGTTTGGGAAGCCCTCTACTCTCTTTC 782
Db
721 TTTCCAGTGTGTGCTTCTGGCTGGGGGAGATAAAGCATGCTGCTCTTCAACAATAC 780
|||||
783 TTTCCAGTGTGTGCTTCTGGCTGGGGGAGATAAAGCATGCTGCTCTTCAACAATAC 842
Db
781 ATGCACAAAAAGTACCGCAGACAGACAAACCGAGAAATTATCATAGAGAGAGGTGAC 840
|||||
843 ATGCACAAAAAGTACCGCAGACAGACAAACCGAGAAATTATCATAGAGAGAGGTGAC 902
Db
841 CACCCCTAAGGGCATTTGAGATGGTGGAAATGATGAATTTCCATTTCTAGATGGGAA 900
|||||
903 CACCCCTAAGGGCATTTGAGATGGTGGAAATGATGAATTTCCATTTCTAGATGGGAA 962
Db
901 CTGGTCCCCCTGGAAAGGAGAGATGATGCCGAGAGATGCCGATTCG 960
|||||
963 CTGGTCCCCCTGGAAAGGAGAGATGATGCCGAGAGATGCCGATTCG 1022
Db
961 AAGGATCTGAAGCAAAACACCCAGAGAGACTTATGATCAGCTGGTGGAGATGCCAAT 1020
|||||
1023 AAGGATCTGAAGCAAAACACCCAGAGAGACTTATGATCAGCTGGTGGAGATGCCAAT 1082
Db
1021 TACTATGCTCTTCTCCACCAAGAGAAAGCCGCTTCTACCGTATGCCAAGCCACTGT 1080
|||||
1083 TACTATGCTCTTCTCCACCAAGAGAAAGCCGCTTCTACCGTATGCCAAGCCACTGT 1142
Db
1081 ATGATGACGCTGGAGGAGCAATATCTGAAAGAAACATGACAGACAGAACCAAGAGGCG 1140
|||||
1143 ATGATGACGCTGGAGGAGCAATATCTGAAAGAAACATGACAGACAGAACCAAGAGGCG 1202
Db
1141 TCCAGCATGAGGAGGTGACACACCGATGAGCCTGAGACTTATTTCCAAAGCTCTCTT 1200
|||||
1203 TCCAGCATGAGGAGGTGACACACCGATGAGCCTGAGACTTATTTCCAAAGCTCTCTT 1262
Db
1201 GACCCATCTTCTTACCAAGTGCCTGGAGAACTGGGGCTGTACTCTGACAGTGTAGAG 1260
|||||
1263 GACCCATCTTCTTACCAAGTGCCTGGAGAACTGGGGCTGTACTCTGACAGTGTAGAG 1322
Db
1261 AAGGGGAGACATGTCACAAAGACATGTATGTGACTACAAAAACAGAGATGTTCTGCC 1320
Db
1323 AAGGGGAGACATGTCACAAAGACATGTATGTGACTACAAAAACAGAGATGTTCTGCC 1382
Db
1321 AATGCAGGGGCTGACTATGATTCACAGAGGGGAGGTTCTTGAAGCCAGAGAGACC 1380
|||||
1383 AATGCAGGGGCTGACTATGATTCACAGAGGGGAGGTTCTTGAAGCCAGAGAGACC 1442
Db
1381 CAGAAAGAGTCTCCGTGGGCAATATTTGATGACGACATTTTGAAGAGATGAACCTTC 1440
|||||
1443 CAGAAAGAGTCTCCGTGGGCAATATTTGATGACGACATTTTGAAGAGATGAACCTTC 1502
Db
1441 TTTTGAAGTTGAGCAATGTCCGATAGAGAGAGACACAGAGAGAGAGGATGCTCCA 1500
|||||
1503 TTTTGAAGTTGAGCAATGTCCGATAGAGAGAGACACAGAGAGAGAGGATGCTCCA 1562
Db
1501 GCAAAATTTAAGAGTCTTCCCTGGGCTGTCTAGCCCTCCCTTGTGTGGGCACA 1560
|||||
1563 GCAAAATTTAAGAGTCTTCCCTGGGCTGTCTAGCCCTCCCTTGTGTGGGCACA 1622
Db
1561 GTTACCATCTTGGAGATGACCATGAGGCAATCTTCACTTTGAATGTATATCTATTCAT 1620
|||||
1623 GTTACCATCTTGGAGATGACCATGAGGCAATCTTCACTTTGAATGTATATCTATTCAT 1682
Db
1621 GTTACCATCTTGGAGATGACCATGAGGCAATCTTCACTTTGAATGTATATCTATTCAT 1680
|||||
1683 GTTACCATCTTGGAGATGACCATGAGGCAATCTTCACTTTGAATGTATATCTATTCAT 1742
Db
1681 ACAGTATCTGTCCTCTTATGAGACATGAGAAAGGACAGCAAGGATGGGCTGAGACTTT 1740
|||||

|||||
1743 ACAGTATCTGTCCTCTTATGAGACATGAGAAAGGACAGCAAGGATGGGCTGAGACTTT 1802
Db
1741 GAAAGACATATGGGAGATTTGGAATTCAGAAATGATGAAGAACTGTGAAGCAATAGGTT 1800
|||||
1803 GAAAGACATATGGGAGATTTGGAATTCAGAAATGATGAAGAACTGTGAAGCAATAGGTT 1862
Db
1801 AAAATGATGATGAGAGAAATACGAAGGCAAGAGAAATTTCTTATTCCTCTGGTGAA 1860
|||||
1863 AAGGTATGATGATGAGAGAAATACGAAGGCAAGAGAAATTTCTTATTCCTCTGGTGAA 1922
Db
1861 CCGAAATGATGAGAACTGGAATATCAGATGTG-----ACAGACAGAAAGCTG 1908
|||||
1923 CCGGATGATGAGAACTGGAATATCAGATGTG-----ACAGACAGAAAGCTG 1982
Db
1909 ACTATGAAAGAGAGAGGCGCAAGAGATATGACAGATGGGAAAGCACTATTTGGTGAA 1968
|||||
1983 ACTATGAAAGAGAGAGGCGCAAGAGATATGACAGATGGGAAAGCACTATTTGGTGAA 2042
Db
1969 CACCCCAACTGAAAGTCAATTTGAAGAGTCTTATGAGTTCAGAGTCAAGACTACGGTGCACA 2028
|||||
2043 CACCCCAACTGAAAGTCAATTTGAAGAGTCTTATGAGTTCAGAGTTCAGAGTCAAGACTAC 2102
Db
2029 CTGATCAGAGAGCAAAACCTGGCTTGTGTGGGAGACCATTTCTGAGAGGACAGTTTC 2088
|||||
2103 CTGATCAGAGAGCAAAACCTGGCTTGTGTGGGAGACCATTTCTGAGAGGACAGTTTC 2162
Db
2089 ATGAGGCGCATCACCGTCACTGTCAGCAGGAGATGAGATGAGATGAATTCGGGGAGAG 2148
|||||
2163 ATGAGGCGCATCACCGTCACTGTCAGCAGGAGATGAGATGAGATGAATTCGGGGAGAG 2222
Db
2149 AAGCTGCGCTCCGCTTACTATGATGATGATGATGATGATGATGATGATGATGATGATG 2208
|||||
2223 AAGCTGCGCTCCGCTTACTATGATGATGATGATGATGATGATGATGATGATGATGATG 2282
Db
2209 TTTGCTGTGTGCCCCCAGAGAGTACTGCAAGGCTGGGCTGCTTCCGCTCTCATC 2268
|||||
2283 TTTGCTGTGTGCCCCCAGAGAGTACTGCAAGGCTGGGCTGCTTCCGCTCTCATC 2342
Db
2269 CTGATCATTTGGCATGCTCAACCGCATATTTGGGAGCTTGGCTGCGCATTTGGCTCAC 2328
|||||
2343 CTGATCATTTGGCATGCTCAACCGCATATTTGGGAGCTTGGCTGCGCATTTGGCTCAC 2402
Db
2329 ATTGCTCTAAGATTCAGTCACAGCTGTGTTTGTGGCATTTGGGACCTCTGCCCCA 2388
|||||
2403 ATTGCTCTAAGATTCAGTCACAGCTGTGTTTGTGGCATTTGGGACCTCTGCCCCA 2462
Db
2389 GATACGTTTGGCAGCAAACTGCTGCCCTCCAGAGATGTATATGCAACGCTCTCATTTGGC 2448
|||||
2463 GATACGTTTGGCAGCAAACTGCTGCCCTCCAGAGATGTATATGCAACGCTCTCATTTGGC 2522
Db
2449 AACGTACGGGCGAGCAACCGCTCAATGTCTTCTGGGCAATCGGCTGTGGCTGTCCGTG 2508
|||||
2523 AACGTACGGGCGAGCAACCGCTCAATGTCTTCTGGGCAATCGGCTGTGGCTGTCCGTG 2582
Db
2509 GCGGCAATCTACTGGGCTCTGCAAGGAGAGATTCACAGTGTGCGGCGGCAACATGTGCC 2568
|||||
2583 GCGGCAATCTACTGGGCTCTGCAAGGAGAGATTCACAGTGTGCGGCGGCAACATGTGCC 2642
Db
2569 TTTCTCCGTACCCCTTTCACCATTTTGTGATCTTGTGATCAGGCTGTCTGTACCGA 2628
|||||
2643 TTTCTCCGTACCCCTTTCACCATTTTGTGATCTTGTGATCAGGCTGTCTGTACCGA 2702
Db
2629 AGGCGGCGGACCTGGGAGGAGAGCTTGGTGGGCGGCGGCTGCAAGCTGCGCACACA 2688
|||||
2703 AGGCGGCGGACCTGGGAGGAGAGCTTGGTGGGCGGCGGCTGCAAGCTGCGCACACA 2762
Db
2689 TGGCTCTTGTGAGGCTGTGGGCTCTACATCTTGTGCAACATGAGGCTGTATTCG 2748
|||||
2763 TGGCTCTTGTGAGGCTGTGGGCTCTACATCTTGTGCAACATGAGGCTGTATTCG 2822
Db
2749 TACATCAAGGGGTTCTAA 2766
|||||

Db 2823 TACATCAAGGGTTCTAA 2840

RESULT 6
LOCUS RNU53420 4854 bp mRNA linear ROD 04-OCT-1996
DEFINITION Rattus norvegicus sodium-calcium exchanger form 3 (NCX3) mRNA,
complete cds.
ACCESSION U53420
VERSION U53420.1 GI:1552525
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4854)
Nicolli,D.A., Quednau,B.D., Qui,Z., Xia,Y.R., Lusis,A.J. and
Phillipson,K.D.
Cloning of a third mammalian Na⁺-Ca²⁺ exchanger, NCX3
J. Biol. Chem. 271 (40), 24914-24921 (1996)
MEDLINE 8798769
PUBMED 2 (bases 1 to 4854)
REFERENCE Nicolli,D.A. and Phillipson,K.D.
AUTHORS Submitted (02-APR-1996) Physiology, University of California, Los
JOURNAL Direct Submission Angeles, 3645 MRLB, 675 Circle Dr. S., Los Angeles, CA 90095-1760,
USA

FEATURES
Source

1. .4854
Location/Qualifiers
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/map="tightly linked to D12Ucla3"
/note="maps to chromosome 12 in mouse and 14q21-31 in
human"
1. .4854
/gene="NCX3"
834. .3617
/gene="NCX3"
/note="similar to human ncx2 product encoded by GenBank
Accession Number X93017"
/codon_start=1
/product="sodium-calcium exchanger form 3"
/protein_id="AAC52817.1"
/db_xref="GI:1552526"

gene
CDS

/translation="MAMRLQPLTSAFLHGLTVFLNLGLRAEGDLRDPVSAGN
NESCSSSDCKEGVILPIWPNPNSLGDITARIIVYFVALIYMLGVSIADRFMASI
EVTISQEREVTIKKPNGETSTIRWNETVSNLTMLALSSAPETILSLIEVCGHF
IADLDPSITVSGAENFMFTIGICVYVDPGEIRKIKHLRFVTAAMGVAYIMLY
MLAVFSPGVVWEGILTFEPVVCVLLAVADKRLLEKKYMKRRYRDKHGIITE
TGEHKGITMDCKMNSHFLDNLPIRBEKVEDESREIRIKLKDCKHPEKDDO
LVBMAITVLSHOKSHAFRIQATRMGTAGNLIKHAEOAKKTASKEVITDEPE
DFASKVFPDSCSYOCLENGCAVLITVVRKGDLSKMYVDYKTEDSANGADYELE
GTVVLPGEFOKEFSVGIIDDDIFEEDEHFFVLSNRYEEDOLEGMPALINSLE
PRAVLASPCVATYTIIDDDHAGIFTEECOTIHVSESGVMEVVLRTSGARGVIVPE
RTVEGTAKGGGGEFEDTGELEKDEKDETITIKTYDEEYRQENFEITALEPKM
ERGISALLSPRYTDRKLMEEREARIAMGCRPVIGENHKELEVIIESEPERSTYDK
LIKRTNALVYGTSHWRDPEALITVSADDEEDSEGERLSCDFVNHFLVEMK
VLPACVPPEYEGHMACFVYSIIGMLTAIIDLASHFCCTIGLDSVAIVAVFENK
TSVPDTPASKAALADVDASIGNVTGSNAVAVFLGIGLAMSVAALYMMQOEFEHY
SAGTAAFSVTLFTIFAFVCLSVLLYRRRPHLGEIDGPRCKLATITWLFVSLMLTVL
FATLEAYCYKGF"

BASE COUNT 1162 a 1216 c 1267 g 1209 t
ORIGIN

Query Match 85.0% Score 2352.4; DB 10; Length 4854;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 2525; Conservative 0; Mismatches 241; Indels 18; Gaps 1;

OY 1 ATGGCGTGGTTAAAGCTTCACCTTCCTTCATTTGGCGTGGTACC 60
|||||

Db 834 ATGGCGTGGTTAAAGCTTCACCTTCCTTCATTTGGCGTGGTACT 893
OY TTTGTCCTTCCTGAATAGGCTTCGAGCAGAGCGTGGTGGTCAAGGAGCTCCAAAGC 120
|||||
Db 894 TTTTGCTCTTCCTGAATAGGCTTCGAGCAGAGCGTGGTGGTCAAGGAGCTCCAAAGC 953
|||||
OY 121 ACAGGGCAAGAAACAATGAGTCCCTGTCAGGGTTCATCGAGCTGCAAGAGAGGTGCATCTG 180
|||||
Db 954 GCAGGACAGAAACAATGAGTCCCTGTCAGGGTTCATCGAGCTGCAAGAGAGGTGCATCTG 1013
|||||
OY 181 CCAATCTGTTACCCGGAGAACCTTCCTTGGGACAAAGATGCCAGAGTTCATGTCTAT 240
|||||
Db 1014 CCAATCTGTTACCCGGAGAACCTTCCTTGGGACAAAGATGCCAGAGTTCATGTCTAT 1073
|||||
OY 241 TTTGTCCTTCCTGAATAGGCTTCGAGCAGAGCGTGGTGGTCAAGGAGCTCCAAAGC 300
|||||
Db 1074 TTTTGCGCCCTGATATATACATGTTCTTGGAGTGTCTATCATTTGCTGACCATTTATGCA 1133
|||||
OY 301 TCTATTGAAGTCATCACCTTCACAGAGAGGAGGTGACAAATTAAAGAACCCAAATGAGAA 360
|||||
Db 1134 TCTATTGAAGTCATCACCTTCACAGAGAGGAGGTGACAAATTAAAGAACCCAAATGAGAG 1193
|||||
OY 361 ACCAGCAACAACCATATTGGGCTCGAATGAACCTGTCTCAACCTGACCCCTTATGACC 420
|||||
Db 1194 ACCAGCAACAACCATATTGGGCTCGAATGAACCTGTCTCAACCTGACCCCTGATGGCC 1253
|||||
OY 421 CTGGGTCCTGCTGCTCGTCAAGATACCTCTTAAATGAGGTGTGGTCATGGGTTTC 480
|||||
Db 1254 CTAGGCTCTTGTGCTCCGGAGATTCCTGCTTAAATGAGGTGTGGTCATGGGTTTC 1313
|||||
OY 481 ATTCGTCGTGATCTGGGACCTTTACCATGTGAGGAGTGCAGCTTCACATGTTTCATC 540
|||||
Db 1314 ATTCGTCGTGATCTGGGACCTTCACCATGTGAGGAGTGCAGCTTCACATGTTTCATC 1373
|||||
OY 541 ATCATTTGCAATCTGTCCTACGTATCCAGAGGAGAGTCCAGATCAACATCACTA 600
|||||
Db 1374 ATCATTTGCAATCTGTCCTACGTATCCAGAGGAGAGTCCAGATCAACATCACTA 1433
|||||
OY 601 CGAGTCTTCTTCATCACCGGCTGTTGAGATATCTTCCCTCATCTGGCTATATGAT 660
|||||
Db 1434 CGAGTCTTCTTTCGACGGCGCTTGGAGCCTCTTTCCTATATTTGGCTCTACATGATC 1493
|||||
OY 661 CTGGCAGTCTTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
|||||
Db 1494 CTGGCAGTCTTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1553
|||||
OY 721 TTTCCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
|||||
Db 1554 TTTCCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1613
|||||
OY 781 ATGCACAAAAAGTACCGCAGACAAACACCGAGGAATTTATCATAGACAGAGGTGAC 840
|||||
Db 1614 ATGCACAAAAAGTACCGCAGACAAACACCGAGGAATTTATCATAGACAGAGGTGAA 1673
|||||
OY 841 CACCTTAAGGCAATGAGATGAGTGGAAAAATGATGAAATTTCTTCTAGATGGGAAC 900
|||||
Db 1674 CACCTTAAGGCAATGAGATGAGTGGAAAAATGATGAAATTTCTTCTAGATGGGAAC 1733
|||||
OY 901 CTGGTGGCCCTGGAAGGAAGAGTGAAGTCCCGCAGAGAGATGATCGGATCTCTC 960
|||||
Db 1734 CTGGTGGCCCTGGAAGGAAGAGTGAAGTCCCGCAGAGAGATGATCGGATCTCTC 1793
|||||
OY 961 AAGGATCTGAAGCAAAAAACACCGAGAGACTTGAAGTACGTGGGTGAGATGGCAAT 1020
|||||
Db 1794 AAGGATCTGAAGCAAAAAACACCGAGAGACTTGAAGTACGTGGGTGAGATGGCAAT 1853
|||||
OY 1021 TACTATGCTCTTTCCACACACAGAGAGCGGCTTCTTACCGTATCCAGGCACTCGT 1080
|||||
Db 1854 TACTATGCTCTTTCCACACACAGAGAGCGGCTTCTTACCGGATCCAGGCACTCGG 1913
|||||
OY 1081 ATGATGACTGGTGCAGGCAATATCTCTGAAGAAACATGACAGAAAGCCAGAGAGCC 1140
|||||
Db 1914 ATGATGACTGGTGCAGGCAATATCTTGAAGAAACATGACAGAGAGCCAGAGAGCC 1973
|||||


```
/gene="S1c8a3"  
/codon_start=1  
/product="sodium/calcium exchanger"  
/protein_id="AL39160.1"  
/db_xref="gi:17432811"  
/translation="MAMRLQPLTSAFLHFLGVLTPFLNCLRAEAGDSQDVSAQN  
NESGSSSDCKEGLVILPIMVPENPSLGDRIKARIYVFAVLIYFLEVSLIADPFMSI  
EVTTSQREVTIKKPNGETSTTIRVWNETVSLTLMALSGSPBELLSTLIECGHF  
IADGLPSTIVGSAANMFIIGICVLIJPDGSTRKIKHFRVFVAAMSIYIMLF  
MLAVSPGVVYQWEGELTLFEFPCVLLAMVADRKLFEYKHKYRIKDHGIIIE  
TEGDHKGIEMDKMMNSHRLDGNFTPLEKEDSREMRITLKLKOLKOPKRDLO  
LYEMANTYALSHOOKRARIQIOTATRMATGAGNIIKHAHQKRTISSMEVITDE  
DFASKVDFPDCSTQCLENGCAVLITVRKRGDLSKIMYVDYKTESDANAGADYELE  
GTVNLKPGETQKEFSVGIIDDDIFEEDHEFVRLSVREEDQLAEGMLPALLNSLP  
PRAVLASPCVAATVLIIDDHAGIIFECODIHVSESIGVMEVRLTSGARGLVIFP  
RVETGAKGGEDFEDAYGELEKDEYVTHIIRIKYIDDAKYNKNYVIEKMGPRV  
DMSVOKALLSPEDVRKLVEEBAKRIAEKMPVLGHEPKLEVIKIKKOEKRSYVD  
KLIKRTNLALYVTHSMRDPFAITVSAGDDEDESGERIPSCFDYMHFLTPFM  
KVLNACVPPEYCPGNACFVNSTLIIGMLATIIIGLASHGCTIGLDSVTAVFVAE  
GTSVPDIFASKAALQDVADASIGNVSGMAVNVELGIGLASVAIYWMAGOEER  
VSAQTIAFSVTLTIFAFVCLSVLLYRRRPHLGEIGRPGKILATTWLFSIMLYI  
LFATLBAVCYIKGF"
```

BASE COUNT 745 a 900 c 988 g 802 t

ORIGIN

Query Match

Best Local Similarity 82.8%; Score 2290.2; DB 10; Length 3435;

Matches 2488; Conservative 0; Mismatches 278; Indels 21; Gaps 1;

```
QY 1 ATGGCGGTGTTAAGTTGACAGCTCTACCTCTGCTCCCTCCATTTTGGGCTGTTACC 60  
DB 603 ATGGCGGTGTTAAGTTGACAGCTCTACCTCTGCTCCCTCCATTTTGGGCTGTTACT 662  
QY 61 TTTGCTGCTTCTGTAAGTGGCTTTCGAGCAGAGGCTGGTGCTCAGGGGAGTCCCAAG 120  
DB 663 TTTTGCTCTTCTGTAAGTGGCTTTCGAGCAGAGGCTGGTGCTCAGGGGAGTCCCAAGT 722  
QY 121 ACAGGGGAGAAACAATGAGTCCCTGTTACAGGGTCAATCGGATCGCAAGAGGGGTGCATCTG 180  
DB 723 GCAGGGGAGAAACAATGAGTCCCTGTTACAGGGTCAATCGGATCGCAAGAGGGGTGCATTTTG 782  
QY 181 CCAATCTGTAACCCGGAGAACCTTCCCTTGGGACAAGATGGCAGGGTCAATGCTAT 240  
DB 783 CCAATCTGTAACCCGGAGAACCTTCCCTTGGGACAAGATGGCAGGGTCAATGCTAT 842  
QY 241 TTTTGCGCCCTGATATATCATGTTCTTGGGGGTGCATCATTTGTCAGCCGCTTCATGGA 300  
DB 843 TTTTGCGCCCTGATATATCATGTTCTTGGGGGTGCATCATTTGTCAGCCGCTTCATGGA 902  
QY 301 TCTATTTGAGTCAATCACCTCTCAAGAGAGGGAGTGAACATTTAGAAACCCCAATGAGAA 360  
DB 903 TCTATTTGAGTCAATCACCTCTCAAGAGAGGGAGTGAACATTTAGAAACCCCAATGAGAA 962  
QY 361 ACCGAGCAACAACATATTGGGCTCGAATGAACCTGTCTCAACCTGACCCCTTATGGCC 420  
DB 963 ACCGAGCAACAACATATTGGGCTCGAATGAACCTGTCTCAACCTGACCCCTTATGGCC 1022  
QY 421 CTGGGCTCTCTGCTCTCGAGATACCTCTCTTAATTTGAGGTGAGTGGCATGGGCTC 480  
DB 1023 CTGGGCTCTCTGCTCTCGAGATACCTCTCTTAATTTGAGGTGAGTGGCATGGGCTC 1082  
QY 481 ATTGCTGTGATCTGGAGACCTTCTACCATTTGAGGAGTGGAGGCTTCAACATGTTTCATC 540  
DB 1083 ATTGCTGTGATCTGGAGACCTTCTACCATTTGAGGAGTGGAGGCTTCAACATGTTTCATC 1142  
QY 541 ATCATTTGCGATCTGTGCTACGTGATCCAGAGCGAGAGACTCGCAAGATCAAGCATCTA 600  
DB 1143 ATCATTTGCGATCTGTGCTACGTGATCCAGAGCGAGAGACTCGCAAGATCAAGCATCTA 1202  
QY 601 CGAGTCTTCTTCATCAGCGGCTTGGAGTATCTTTGCTACATCATGGCTCTATATGATT 660  
DB 1203 CGAGTCTTCTTCATCAGCGGCTTGGAGTATCTTTGCTACATCATGGCTCTATATGATT 1262
```

```
QY 661 CTGGCAGTCTTCTCCCTGCTGTGCTCCAGGTTTGGAGAGCCCTCTCACTCTCTCTTC 720  
DB 1263 CTGGCAGTCTTCTCTCTGCTGTGCTCCAGGTTTGGAGAGCCCTCTCACTCTCTCTTC 1322  
QY 721 TTTTCCAGTGTGCTCTCTCTGCTGTGCTGGGCTGAGATTAAGACAGTGCCTCTCAAAATAC 780  
DB 1323 TTTTCCAGTGTGCTCTCTCTGCTGTGCTGGGCTGAGATTAAGACAGTGCCTCTCAAAATAC 1382  
QY 781 ATGCACAAAAAGTACCCGACAGACAAACACCCGAGGAATTTATCATAGACAGAGGGTAC 840  
DB 1383 ATGCACAAAAAGTACCCGACAGATTAACACCCGAGGAATTTATCATAGACAGAGGGTAC 1442  
QY 841 CACCTTAAGGCGATTTGAGATGATGGGAAAAATGTAATTTCCATTTTCTATAGATGGAC 900  
DB 1443 CACCTTAAGGCGATTTGAGATGATGGGAAAAATGTAATTTCTCTTTCTATAGATGGAC 1502  
QY 901 CTGGTGGCCCTGGAAGGAAGGATGATGAGTCCGACAGAGATGATCCGATCTC 960  
DB 1503 TTTACACCTTTGGAAGGAAGGATGATGATGATCTCGACAGGAATGATCCGATCTC 1562  
QY 961 AAGGATCTGAAGCAAAAAACACCCGAGAGAGCTTATGATCAGCTGTGTGAGATGGCAAT 1020  
DB 1563 AAGGATCTGAAGCAAAAAACACCCGAGAGAGCTTATGATCAGCTGTGTGAGATGGCAAT 1622  
QY 1021 TACTATGCTCTTTTCCACACACAGAGAGCCGCGCTTTTACGATATCCAGCCACTGCT 1080  
DB 1623 TACTATGCTCTTTTCCACACACAGAGAGCCGCGCTTTTACGATATCCAGCCACTGCT 1682  
QY 1081 ATGATGACTGCTGACGCAATATCCCTGAAGAAATGATCAGACAGAACCAAGCAAGAGCC 1140  
DB 1683 ATGATGACTGCTGACGCAATATCCCTGAAGAAATGATCAGACAGAACCAAGCAAGAGCC 1742  
QY 1141 TCCAGCATGAGCAGAGGTGACACACAGATGAGCCTTATTTATTTCAAGGCTCTCTTT 1200  
DB 1743 TCCAGCATGAGCAGAGGTGACATCCGATGAGCAGGAGACTTTGGCTCTTAAGTCTTCTTT 1802  
QY 1201 GACCCATGTTCTTACAGAGTGCCTGGAGAACTGTGGGCTGTACTCTGTACAGTGTGAGG 1260  
DB 1803 GACCCATGTTCTTATCAGTGTGCCTGGAGAACTGTGAGAACTGTGCTGCTGACCTGTGTGAGG 1862  
QY 1261 AAAGGGGAGACATGTCMAAGAACCATATGATGTGACATCAAAACAGAGAGGCTTCGCC 1320  
DB 1863 AAAGGGGAGATATATCAAGAACCATATGATGTGACATCAAAACAGAGAGGCTTCGCC 1922  
QY 1321 AATGACGGGCTGACTATGAGTTTACAGAGGCGACGSGTGTGTTGAGACCAAGAGAGACC 1380  
DB 1923 AATGACGGGCTGACTATGAGTTTACAGAGGCGACGSGTGTGTTGAGACCAAGAGAGACC 1982  
QY 1381 CAGAGGAGTTCCTCGTGGGCATATTTGATGACGACATTTTGTGAGAGATGAACACTTC 1440  
DB 1983 CAGAGGAGTTCCTCGTGGGCATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 2042  
QY 1441 TTTTGTAGGTTGACCATATGCTCCGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
DB 2043 TTTTGTAGGTTGACCATATGCTCCGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2102  
QY 1501 GCAATATTCAACAGACTTCTCCCTTCTCGGGCTTCTCTAGCTCCCTTGTGTGGCCACA 1560  
DB 2103 GCAATATTCAACAGACTTCTCCCTTCTCGGGCTTCTCTAGCTCCCTTGTGTGGCCACA 2162  
QY 1561 GTTACCATCTTGGATGATGACATGACAGGACTCTTCACTTTTGAATGATGATGATGAT 1620  
DB 2163 GTTACCATCTTGGATGATGACATGACAGGACTCTTCACTTTTGAATGATGATGATGATGAT 2222  
QY 1621 GTGAGTGAAGTATGTTGTTATGAGAGTCAAGGTTTGTAGGACATGATGATGATGATGAT 1680  
DB 2223 GTGAGTGAAGTATGTTGTTATGAGAGTCAAGGTTTGTAGGACATGATGATGATGATGATGAT 2282  
QY 1681 ACAATCATGCTCCCTTTAGAGCAGTGAAGAGGACCAAGAGGTGCGGTGAGAGATTT 1740  
DB 2283 ACAATCATGCTCCCTTTAGAGCAGTGAAGAGGACCAAGAGGTGCGGTGAGAGATTT 2342  
QY 1741 GAAGCACAATATGGGAGTGTGAATTCAGAAATGATGAACACTGTGAACCAATTAAGGTT 1800
```

```

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 2343 GAAAGTGCATATGGGAGCTGGAGTTCAAGATGATGAACAGCTCAAAACATTCACATC 2402
Oy 1801 AAAATAGTAGAGAGAGAAATACGAAGGCAAGAAATTTCTTCAATTCCTTGGTGA 1860
Db 2403 AAGGTAAATGATGATAGGCGATGAGAAACAAAGAAATTTAGTCAATGATGATGAGG 2462
Oy 1861 CCGAAATGATGGAACGTGAATAT-----CAATGTGACAGAC 1899
Db 2463 CCCCAGCATGGTGGATATGAGTGTTCAGAAAGCGCTCTGTATCTTCCAAAGTGACAGAC 2522
Oy 1900 AGCAAGCTACTATGAGAGAGAGAGAGAGAGAGAGATGAGAGATGAGAGAGAGAGAG 1959
Db 2523 AGCAAGCTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGATGAGAGATGAGAGAGAGAG 2582
Oy 1960 TTGGGTGAACACCCCAAACTAGAGTCAATGAGAGTCTTATGATGATGATGATGATG 2019
Db 2583 TTGGGTGAACACCCCAAACTAGAGTCAATGAGAGTCTTATGATGATGATGATGATG 2642
Oy 2020 GTGGACAACTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2079
Db 2643 GTGGATTAACCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2702
Oy 2080 GACCAAGTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2139
Db 2703 GACCAAGTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2762
Oy 2140 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2199
Db 2763 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2822
Oy 2200 AAGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2259
Db 2823 AAGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2882
Oy 2260 GTCTCCATCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2319
Db 2883 GTCTCCATCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2942
Oy 2320 GGGTGCACCATGTTGTTCAAAAGTTCACAGCTGTGTGTGTGTGTGTGTGTGTGTGT 2379
Db 2943 GGGTGCACCATGTTGTTCAAAAGTTCACAGCTGTGTGTGTGTGTGTGTGTGTGTGT 3002
Oy 2380 TCTGTCCAGATGATGTTTGCAGCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2439
Db 3003 TCTGTCCAGATGATGTTTGCAGCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3062
Oy 2440 TCCATTGGCAAGCTGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2499
Db 3063 TCCATTGGCAAGCTGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3122
Oy 2500 TGGTCCGTGGCCGCCATCTACTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2559
Db 3123 TGGTCCGTGGCCGCCATCTACTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3182
Oy 2560 ACACATGGCTTCCGCTACACCTCTACACATTTGCAATTTGCAATTTGCAATTTGCA 2619
Db 3183 ACCTGTGGCTTCCGCTACACCTCTCTTTCACCATTTTGCATTTTGCCTCACTGTGCTC 3242
Oy 2620 TTGTACGGAAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2679
Db 3243 TTGTATCTGTGGGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3302
Oy 2680 GCCACAAACATGAGCTTTGTGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2739
Db 3303 GCCACAAACATGAGCTTTGTGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3362
Oy 2740 GCCTATTGCTACATCAAGGGGTTCTAA 2766
Db 3363 GCCTATTGCTACATCAAGGGGTTCTGA 3389

```

RESULT 8

```

HSNCX22
LOCUS HSNCX22 2534 bp DNA linear PRI 12-NOV-2000
DEFINITION Homo sapiens partial SLC8A3 gene for solute carrier family 8
(sodium/calcium exchanger), member 3 (SLC8A3), exon 2.
ACCESSION X93017
VERSION X93017.1 GI:1067133
KEYWORDS SLC8A3 gene; sodium-calcium exchanger.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2534)
Kraev A., Chumakov, I. and Carefoli, E.
The organization of the human gene NCX1 encoding the sodium-calcium
exchanger
Genomics 37 (1), 105-112 (1996)
JOURNAL MEDLINE 97079665
PUBMED 8921376
REFERENCE 2 (bases 1 to 2534)
Kraev, A.S.
Direct Submission
JOURNAL Submitted (14-NOV-1995) A.S. Kraev, Swiss Federal Institute of
Technology, Laboratory of Biochemistry III, Universitaetstr. 16,
Zurich, CH-8092, SWITZERLAND
Similar to X91213.
COMMENT
FEATURES
source
1..2534
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/map="q24.1"
/cell_line="W138"
/cell_type="fibroblast"
/tissue_type="lung"
/clone_lib="Stratagene genomic #946204"
/gene="SLC8A3"
281..2126
/gene="SLC8A3"
281..2126
/exon
gene
281..2126
/exon
BASE COUNT 602 a 595 c 644 g 693 t
ORIGIN
Query Match 64.6%; Score 1786.4; DB 9; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 AAGCGGCTTAAGGTTCAGAGCTTCACCTGCGCTCTCCATTTGGGCTGGTTAC 60
Db 343 ATGGCGGGTTAAGGTTCAGAGCTTCACCTGCGCTCTCCATTTGGGCTGGTTAC 402
Oy 61 TTGTGCTCTCTCGAATGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 403 TTGTGCTCTCTCGAATGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 462
Oy 121 ACAGGCGAACAATGAGTCTGTTCAAGGCTGATCGGACTGCAAGAGAGGTTGATCTTG 180
Db 463 ACAGGCGAACAATGAGTCTGTTCAAGGCTGATCGGACTGCAAGAGAGGTTGATCTTG 522
Oy 181 CCAATCTGTATCCCGGAGAACCTTCCCTTGGGAGACAAGATTCGAGGCTATTTGTTAT 240
Db 523 CCAATCTGTATCCCGGAGAACCTTCCCTTGGGAGACAAGATTCGAGGCTATTTGTTAT 582
Oy 241 TTGTGGCCCTGATATATCATGTTCTTGGGCTGATCATATTCGACCTTCATGAGCA 300
Db 583 TTGTGGCCCTGATATATCATGTTCTTGGGCTGATCATATTCGACCTTCATGAGCA 642
Oy 301 TCTATTGAGTCAATCACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 643 TCTATTGAGTCAATCACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 702

```

```

QY 361 ACAGACACACACATATTCGGGTCTGGAATGAACCTGTCTCCAACTGACCCCTTATGACC 420
    |||
Db 703 ACCGACACACACATATTCGGGTCTGGAATGAACCTGTCTCCAACTGACCCCTTATGACC 762
QY 421 CTGGGTCCTCTGCTCCGAGATCTCTCTTAAATGAGGTGTGGTGCATGGGTTC 480
    |||
Db 763 CTGGGTCCTCTGCTCCGAGATCTCTCTTAAATGAGGTGTGGTGCATGGGTTC 822
QY 481 ATTGCTGTGATCTGGGACCTTCTACCATGTTAGGAGTGCAGCCCTTCAACATGTTATC 540
    |||
Db 823 ATTGCTGTGATCTGGGACCTTCTACCATGTTAGGAGTGCAGCCCTTCAACATGTTATC 882
QY 541 ATCATTTGGCATCTGTCTCTACGTATCCAGACGGAAGACTCCGAAGATCAACATCTA 600
    |||
Db 883 ATCATTTGGCATCTGTCTCTACGTATCCAGACGGAAGACTCCGAAGATCAACATCTA 942
QY 601 CGAGTCTTCTTCATCACCAGGCTTGAGATCTTGGCTACATCTGGCTATATGATT 660
    |||
Db 943 CGAGTCTTCTTCATCACCAGGCTTGAGATCTTGGCTACATCTGGCTATATGATT 1002
QY 661 CTGGCAGTCTTCTCCCTGGGTGTGTCAGGTTTGGGAAGGCTCTCACTCTTCTTC 720
    |||
Db 1003 CTGGCAGTCTTCTCCCTGGGTGTGTCAGGTTTGGGAAGGCTCTCACTCTTCTTC 1062
QY 721 TTTTCACTGTGTCTCTTCTGCGCTGGGTGGCAGATTAACGATCTCTTCTACAAATAC 780
    |||
Db 1063 TTTTCACTGTGTCTCTTCTGCGCTGGGTGGCAGATTAACGATCTCTTCTACAAATAC 1122
QY 781 ATGCACAAAAAGTACGCGACAGACAAACCGAGAAATTATCATAGAGACAGAGGAGAC 840
    |||
Db 1123 ATGCACAAAAAGTACGCGACAGACAAACCGAGAAATTATCATAGAGACAGAGGAGAC 1182
QY 841 CACCTAAGGCGCATTTGATGATGATGGGAAATGATGAATTCATCTTCTTCTAGATGGGAC 900
    |||
Db 1183 CACCTAAGGCGCATTTGATGATGATGGGAAATGATGAATTCATCTTCTTCTAGATGGGAC 1242
QY 901 CTGTGTCCTCTGGAAGGAAAGAGTGAATGATCCCGCAGAGATGATCCGATCTTC 960
    |||
Db 1243 CTGTGTCCTCTGGAAGGAAAGAGTGAATGATCCCGCAGAGATGATCCGATCTTC 1302
QY 961 AAGGATCTGAAGCAAAAAACCCGAGAGAGACTTATACAGCGTGGAGATGGCAAT 1020
    |||
Db 1303 AAGGATCTGAAGCAAAAAACCCGAGAGAGACTTATACAGCGTGGAGATGGCAAT 1362
QY 1021 TACTATGCTCTTCTCCACCAACAGAGAGCGCGCTTCTACCTATCCATCAAGCCATCTGT 1080
    |||
Db 1363 TACTATGCTCTTCTCCACCAACAGAGAGCGCGCTTCTACCTATCCATCAAGCCATCTGT 1442
QY 1081 ATGATGACTGTGTCAGGCAATATCTCTGAAGAATCATGACAGCAAGACCAAGAGGCC 1140
    |||
Db 1423 ATGATGACTGTGTCAGGCAATATCTCTGAAGAATCATGACAGCAAGACCAAGAGGCC 1482
QY 1141 TTCAGCATGAGCGAGGTGACACACCGATGAGCGTGTATTTTCCAGAGCTTCTTT 1200
    |||
Db 1483 TTCAGCATGAGCGAGGTGACACACCGATGAGCGTGTATTTTCCAGAGCTTCTTT 1542
QY 1201 GACCCATGTTCTTACCACTGCTCTGAGAACTGTGGGCTCTACTCTGACAGTGTGAG 1260
    |||
Db 1543 GACCCATGTTCTTACCACTGCTCTGAGAACTGTGGGCTCTACTCTGACAGTGTGAG 1602
QY 1261 AAGGGGAGACATGTCAAAAGACCATGTATGTGACATCAAAAACAGAGATGTTGCC 1320
    |||
Db 1603 AAGGGGAGACATGTCAAAAGACCATGTATGTGACATCAAAAACAGAGATGTTGCC 1662
QY 1321 AATGACAGGGGCTGACTGTAGTTTACAGAGGACCGGTGTTCTGAAGCCAGAGAAACC 1380
    |||
Db 1663 AATGACAGGGGCTGACTGTAGTTTACAGAGGACCGGTGTTCTGAAGCCAGAGAAACC 1722
QY 1381 CAGAGAGAGTCTTCCGTGGGCATTAATGATGACAGACATTTTGTGAGAGATGAACATCTC 1440
    |||
Db 1723 CAGAGAGAGTCTTCCGTGGGCATTAATGATGACAGACATTTTGTGAGAGATGAACATCTC 1782
QY 1441 TTTGTAAAGTTGAGCAATGTCCGCATAGAGAGAGACGACAGAGAGAGGAGATGCCCTCA 1500

```

```

Db 1783 TTTGTAAAGTTGAGCAATGTCCGCATAGAGAGAGACGACAGAGAGGAGATGCCCTCA 1842
QY 1501 GCATATTTCAACAGCTCTTCCCTTGCCTGCGGCTGTCTTACGCTCCCTTGTGTGGCACA 1560
    |||
Db 1843 GCATATTTCAACAGCTCTTCCCTTGCCTGCGGCTGTCTTACGCTCCCTTGTGTGGCACA 1902
QY 1561 GTTACCATCTTGGATGATGACATGACAGGATCTTCACTTTTGAATGTGATTAATTCAT 1620
    |||
Db 1903 GTTACCATCTTGGATGATGACATGACAGGATCTTCACTTTTGAATGTGATTAATTCAT 1962
QY 1621 GTCACTGAGATATTGGTGTATGAGAGTCAAGGTTCTGGGACATGATGATGATGATGAT 1680
    |||
Db 1963 GTCACTGAGATATTGGTGTATGAGAGTCAAGGTTCTGGGACATGATGATGATGATGAT 2022
QY 1681 ACACTGATCGTCCCTTTAGACAGTGAAGAGGACAGCAGGAGGAGGAGGATGATGAT 1740
    |||
Db 2023 ACACTGATCGTCCCTTTAGACAGTGAAGAGGACAGCAGGAGGAGGAGGATGATGAT 2082
QY 1741 GAAGACACATATGGGAGTGGAAATTCAGAAATGATGAACCTGTGAAA 1788
    |||
Db 2083 GAAGACACATATGGGAGTGGAAATTCAGAAATGATGAACCTGTGTAA 2130

```

```

RESULT 9
AX476820 126512 bp DNA linear PAT 12-AUG-2002
LOCUS
Sequence 3 from Patent WO233086.
DEFINITION
AX476820
ACCESSION
VERSION
AX476820.1 GI:22216099
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and
Beasley,E.M.
TITLE
Isolated human transporter proteins, nucleic acid molecules
encoding human transporter proteins, and uses thereof
JOURNAL
Patent: WO 0233086-A.3 25-APR-2002;
PE Corporation (NY) (US)
FEATURES
source
1..126512
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 35679 a 27106 c 27550 g 36176 t 1 others
ORIGIN

```

```

Query Match 64.5%; Score 1784.8; DB 6; Length 126512;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGCGCTGTGTTAAGTTGACAGCTCTACCTCTGCTCTCTCATTTTGGGCTGTGACC 60
    |||
Db 2010 ATGCGCTGTGTTAAGTTGACAGCTCTACCTCTGCTCTCTCATTTTGGGCTGTGACC 2069
QY 61 TTTGTGCTCTTCCGATGAGTGTCTGAGAGAGGCTGTGGCTCAGAGGAGCTGCCAAGC 120
    |||
Db 2070 TTTGTGCTCTTCCGATGAGTGTCTGAGAGAGGCTGTGGCTCAGAGGAGCTGCCAAGC 2129
QY 121 ACAAGGACAGAAATGAGTCTGTTCAGGGTCAATCGAGCTGCAAGAGAGGCTGATCTCTG 180
    |||
Db 2130 ACAAGGACAGAAATGAGTCTGTTCAGGGTCAATCGAGCTGCAAGAGAGGCTGATCTCTG 2189
QY 181 CCAATCTGTACCCGGAAGAACCTTCTCTTGGGAGCAAGATTGCGAGGATCTGTCTAT 240
    |||
Db 2190 CCAATCTGTACCCGGAAGAACCTTCTCTTGGGAGCAAGATTGCGAGGATCTGTCTAT 2249
QY 241 TTTGTGCGCTGATATCATGTTCTGTTGGGTGTCATCTGCTGACCGCTTCATGAGCA 300
    |||
Db 2250 TTTGTGCGCTGATATCATGTTCTGTTGGGTGTCATCTGCTGACCGCTTCATGAGCA 2309

```

Qy 301 TCTATTGAGTCATCATCCTCTCAAGAGAGGAGTGAACATTAAGAAACCCAAATGAGAGA 360
Db 2310 TCTATTGAGTCATCATCCTCTCAAGAGAGGAGTGAACATTAAGAAACCCAAATGAGAGA 2369
Qy 361 ACCAGCACACCACTATTGCGGCTCGAATGAACCTGTCTCCACCTGACCTTATGGCC 420
Db 2370 ACCAGCACACCACTATTGCGGCTCGAATGAACCTGTCTCCACCTGACCTTATGGCC 2429
Qy 421 CTGGGTCCTCTGCTCCCTGAGATTAATCTCTTAAATGAGGTGTGTGATCGGTTTC 480
Db 2430 CTGGGTCCTCTGCTCCCTGAGATTAATCTCTTAAATGAGGTGTGTGATCGGTTTC 2489
Qy 481 ATTGCTGTGATCTGGGACCTTCTACATTTGAGGAGTGCAGCTTAAACATGTTTCATC 540
Db 2490 ATTGCTGTGATCTGGGACCTTCTACATTTGAGGAGTGCAGCTTAAACATGTTTCATC 2549
Qy 541 ATCATTTGCATCTGTCTTACGTATCCAGACGAGAGACTCGCAAGATCAAGCATCTA 600
Db 2550 ATCATTTGCATCTGTCTTACGTATCCAGACGAGAGACTCGCAAGATCAAGCATCTA 2609
Qy 601 CGAGCTCTCTTCATACAGCGCTGTGAGATATCTTGGCTACATCTGGCTCTATATGAT 660
Db 2610 CGAGCTCTCTTCATACAGCGCTGTGAGATATCTTGGCTACATCTGGCTCTATATGAT 2669
Qy 661 CTGGGAGCTTCTCCCTGCTGTGTGCTCCAGGTTTGGAGAGGCTCTCCTCTCTTCTTC 720
Db 2670 CTGGGAGCTTCTCCCTGCTGTGTGCTCCAGGTTTGGAGAGGCTCTCCTCTCTTCTTC 2729
Qy 721 TTTCCAGTGTGTCTCTTCTGCGCTGGGTCGAGATTAACGACTGCTCTTACAAATAC 780
Db 2730 TTTCCAGTGTGTCTCTTCTGCGCTGGGTCGAGATTAACGACTGCTCTTACAAATAC 2789
Qy 781 ATGCACAAAAAGTACCGACAGACAAACACGAGAAATTAATATAGACACAGAGGTGAC 840
Db 2790 ATGCACAAAAAGTACCGACAGACAAACACGAGAAATTAATATAGACACAGAGGTGAC 2849
Qy 841 CACCCTAAGGGCATTGAGATGGATGGAAAAATGATGAATCCCATTTCTAGATGGAAAC 900
Db 2850 CACCCTAAGGGCATTGAGATGGATGGAAAAATGATGAATCCCATTTCTAGATGGAAAC 2909
Qy 901 CTGGTGGCCCTGGAAGGAGAGAGTGAATGATCCCGACAGAGATGATCCGATTTCTC 960
Db 2910 CTGGTGGCCCTGGAAGGAGAGAGTGAATGATCCCGACAGAGATGATCCGATTTCTC 2969
Qy 961 AAGATCTGAAGCAAAAAACCCCAAGAAAGCATTAAGTACAGTGTGAGATGGCCAAAT 1020
Db 2970 AAGATCTGAAGCAAAAAACCCCAAGAAAGCATTAAGTACAGTGTGAGATGGCCAAAT 3029
Qy 1021 TACTATGCTCTTCCACCAACAGAAAGCCGCGCTTCTACCGTATGCCAAGCCACTGCT 1080
Db 3030 TACTATGCTCTTCCACCAACAGAAAGCCGCGCTTCTACCGTATGCCAAGCCACTGCT 3089
Qy 1081 ATGATGACTGCTGAGGCAATATCTTGAAGAAACATGACGACGAACAAGCCAAAGAGCC 1140
Db 3090 ATGATGACTGCTGAGGCAATATCTTGAAGAAACATGACGACGAACAAGCCAAAGAGCC 3149
Qy 1141 TCCAGCATGAGGAGAGTGCACACCCATGAGCTTGAAGACTTATTTCCAAAGTCTTTCT 1200
Db 3150 TCCAGCATGAGGAGAGTGCACACCCATGAGCTTGAAGACTTATTTCCAAAGTCTTTCT 3209
Qy 1201 GACCATGTTCTTACAGTGCCTGGAGAACTGTGGGGCTGATCTGCTGACATGGTGAGG 1260
Db 3210 GACCATGTTCTTACAGTGCCTGGAGAACTGTGGGGCTGATCTGCTGACATGGTGAGG 3269
Qy 1261 AAAGGGGAGACATGTCAAAAGACATGTATGTGACATCAAAAACAGAGATGTTCTGCG 1320
Db 3270 AAAGGGGAGACATGTCAAAAGACATGTATGTGACATCAAAAACAGAGATGTTCTGCG 3329
Qy 1321 AATGAGGGGCTGACTATGAGTTCACAGAGGCGACAGGTGTTCTTAAGCCAGAGAGAC 1380
Db 3330 AATGAGGGGCTGACTATGAGTTCACAGAGGCGACAGGTGTTCTTAAGCCAGAGAGAC 3389
Qy 1381 CAGAAGAGATTCTCCGTGGGCAATAATTGATGACGACATTTTTCAGAGAGATGAACACTTC 1440

Db 3390 CAGAAGAGATTCTCCGTGGGCAATAATTGATGACGACATTTTTCAGAGAGATGAACACTTC 3449
Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCAATAGAGAGAGACACCCAGAGAGGGGATGCCCTCA 1500
Db 3450 TTTGTAAGGTTGAGCAATGTCCGCAATAGAGAGAGACACCCAGAGAGGGGATGCCCTCA 3509
Qy 1501 GCAATATTCACAGTCCCTTGGCTGGGCTGTGCTGATAGCTCCCTGCTGTGGCCACA 1560
Db 3510 GCAATATTCACAGTCCCTTGGCTGGGCTGTGCTGATAGCTCCCTGCTGTGGCCACA 3569
Qy 1561 GTTACCATCTTGGATGATGACCATGACGACATCTTCACTTTGAATGATATCTATTCAT 1620
Db 3570 GTTACCATCTTGGATGATGACCATGACGACATCTTCACTTTGAATGATATCTATTCAT 3629
Qy 1621 GTCAGTGAGAGTATTTGTGTATATGAGGTCAAGGTTCTGCGGACATCAAGTCCCGGGGT 1680
Db 3630 GTCAGTGAGAGTATTTGTGTATATGAGGTCAAGGTTCTGCGGACATCAAGTCCCGGGGT 3689
Qy 1681 ACAGTCATCGTCCCTTTAAGACAGTGAAGGACAGCCAAAGGTGGCGGTGAGACTTT 1740
Db 3690 ACAGTCATCGTCCCTTTAAGACAGTGAAGGACAGCCAAAGGTGGCGGTGAGACTTT 3749
Qy 1741 GAAGACACATATGGGAGTGGATTCAGAAATGATGAACATGTGAAA 1788
Db 3750 GAAGACACATATGGGAGTGGATTCAGAAATGATGAACATGTGAAA 3797
RESULT 10
AF508982
LOCUS
DEFINITION Homo sapiens Na+/Ca2+ exchanger isoform 3 (SLC8A3) gene, promoter
region and complete cds.
VERSION AF508982
KEYWORDS
SOURCE human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 145118)
Gabbellini, N., Bortoluzzi, S., Danieli, G.A. and Carafoli, E.
CONTROL OF THE Na+/Ca2+ EXCHANGER 3 PROMOTER BY cAMP AND Ca2+ IN
DIFFERENTIATING NEURONS
UNPUBLISHED
2 (bases 1 to 145118)
Gabbellini, N., Bortoluzzi, S., Danieli, G.A. and Carafoli, E.
THE HUMAN Na+/Ca2+ EXCHANGER 3 GENE (SLC8A3) AND SPLICED ISOFORMS
UNPUBLISHED
3 (bases 1 to 145118)
Gabbellini, N., Bortoluzzi, S., Danieli, G.A. and Carafoli, E.
DIRECT SUBMISSION
Submitted (02-MAY-2002) Department of Biology, University of
Padova, via G. Colombo 3, Padova, PD 35131, Italy
FEATURES
SOURCE
1..145118
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q24.2"
1..145118
/gene="SLC8A3"
1..263
/gene="SLC8A3"
TATA_signal
236..241
/gene="SLC8A3"
/gene="SLC8A3"
join(264..955,20853..22698,128396..128499,133522..133539,
137221..137345,138228..138327,140293..140568,
143012..145118)
/gene="SLC8A3"
/product="Na+/Ca2+ exchanger isoform 3"
join(264..955,20853..20914)
/gene="SLC8A3"
5'UTR

CDS
join(20915..22698,128396..128499,133522..133539,
137221..137345,138228..138327,140293..140568,
143012..143388)
/gene="SLC8A3"
/note="NCX3: expressed in excitable cells of brain,
retina, and skeletal muscle"
/codon_start=1
/product="Na+/Ca2+ exchanger isoform 3"
/protein_id="AA09095.1"
/db_xref="GI:22087483"
/translation="MAMRLQPLTSAFLHRLVTVFLFNLGRLAEGSGSDVPSGON
NSGSSSPCKEGVILPIKWPENSPISGDKIARIYVFAVLIYFELVSIADREMAST
EYTSQEREYTIKKPNEGSTTIRIWNSTVSLTLMALSSAPETLLSLIECGHF
IAGDLSPSTVSAAPNMFIIIGICVYPIIDETRIKILRVEFTIAAASIFAYILY
MLIAYSPGVVWEGLLTLFFPVCVLLAWADKRLKYKMKKRYRDKHNYLIE
TEGDHKGIEMDGKMNHSLDNLVPLEKREDEBERMIRLKOJOKHPEKDDO
LEVEMANYVALSHOOKSRAFYRIQATRMNGAGILKKHNAEOAKSSASEVHTDE
DPLSKYFDPDSCYCCLENGAVILTYVRGSDMSKMYDYKTEDGSNAGADYETE
GTVVLLKPGETOKESVGIIDDDIFEEDEHFVRLSNVLEEOPREGMPLFNSLPL
PRAVLASPCVAVVTIIDDHAGIFTEECSTIHVSESIGVMEVKVLTSGARGVIVP
RVEGTAKSGGDEDETYGELEKNDYKTIKRVKIVDEEYERQENFIALGEPKM
ERGISALLSPDYDRLKLMEEBEAKRIEMGKPVYGEHKLVEIIEEYHEFTVDK
LIKKTMLALVGHSMRDQMEATVYSAAGDEDESGSERLPSCDYVMHPLTVMK
VLFACYPTEPYCHGNACFVASTIIIGMLTAIIGDLSHSCITLIDSTYAVYFARG
TSVPDTPASKAALDQVADASTIGNVTSNAVNFGLGLANSVAALVWLGQERHV
SAGTLAFSVTLFTIFAFVCIIVLLYRRRLHGLGELGPRCKLATMFLSMLLYIL
FATLEAFVCIYKGF"
143389..145118
/gene="SLC8A3"
145089..145094
polyA_signal
BASE COUNT 40560 a 31471 c 31781 g 41306 t
ORIGIN
Query Match 64.5% Score 1784.8: DB 9: Length 145118;
Best Local Similarity 99.98: Pred. No. 0;
Matches 1786: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCGGTGTTAAGTTGACGCTCTCAGCTGCTCCCTCCATTTTGGGCTGTTACC 60
DB 20915 ATGGCGGTGTTAAGTTGACGCTCTCAGCTGCTCCCTCCATTTTGGGCTGTTACC 20974
QY 61 TTTGTGCTCTTCTGATGATGTCCTTTCGAGCAGAGGCTGTGCTCAGGGGACGTGCCAAC 120
DB 20975 TTTGTGCTCTTCTGATGATGTCCTTTCGAGCAGAGGCTGTGCTCAGGGGACGTGCCAAC 21034
QY 121 ACAGGCGAACAATGATGTCCTGTTCAGGCTCATCGAGCTGCAAGGAGGGGTGCATCTG 180
DB 21035 ACAGGCGAACAATGATGTCCTGTTCAGGCTCATCGAGCTGCAAGGAGGGGTGCATCTG 21094
QY 181 CCAATCTGTACCCGGAGAACCTTCCCTTGGGGACAAAGTTCGACAGGCTCATTTGTTCTAT 240
DB 21095 CCAATCTGTACCCGGAGAACCTTCCCTTGGGGACAAAGTTCGACAGGCTCATTTGTTCTAT 21154
QY 241 TTTGTGCGCTGATATACATGTTCTTGGGGTCCATCATTTGCTGACCGCTTCATGCGCA 300
DB 21155 TTTGTGCGCTGATATACATGTTCTTGGGGTCCATCATTTGCTGACCGCTTCATGCGCA 21214
QY 301 TCTATTGAAGTCATCACTCTCAAGAGAGGAGGTGACATTAAGAAACCAACGAGAGAA 360
DB 21215 TCTATTGAAGTCATCACTCTCAAGAGAGGAGGTGACATTAAGAAACCAACGAGAGAA 21274
QY 361 ACCAGCACAACCACTATTCCGCTCTGGAAATGAAGACTGTCCAAACGACGACCTTATGGCC 420
DB 21275 ACCAGCACAACCACTATTCCGCTCTGGAAATGAAGACTGTCCAAACGACGACCTTATGGCC 21334
QY 421 CTGGGTTCTCTGCTCTGAGTACTCTCTCTTTAATTGAGGTGTGTGTCATGGGTTCC 480
DB 21335 CTGGGTTCTCTGCTCTGAGTACTCTCTCTTTAATTGAGGTGTGTGTCATGGGTTCC 21394
QY 481 ATTGCTGTGATCTGGGACCTTACCATTTGTAGGAGTGCACACCTTCAACATGTTTCATC 540
DB 21395 ATTGCTGTGATCTGGGACCTTACCATTTGTAGGAGTGCACACCTTCAACATGTTTCATC 21454

QY 541 ATCATTTGGCATCTGTGTCTACAGTGATCCAGACGAGAGACTGCGACAGATCAAGCATCTA 600
DB 21455 ATCATTTGGCATCTGTGTCTACAGTGATCCAGACGAGAGACTGCGACAGATCAAGCATCTA 21514
QY 601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCCTACATCTGGCTCTATATGATT 660
DB 21515 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCCTACATCTGGCTCTATATGATT 21574
QY 661 CTGGCAGTCTTCCGCCCTGTGTGTGTCAGGTTCAGGAGGAGGCTCCCTCACTCTCTTCTTC 720
DB 21575 CTGGCAGTCTTCCGCCCTGTGTGTGTCAGGTTCAGGAGGAGGCTCCCTCACTCTCTTCTTC 21634
QY 721 TTTCCAGTGTGTCTCTTCTGCGCTGGGTGGCAGATTAACGACTGCTCTTCAAAATAC 780
DB 21635 TTTCCAGTGTGTCTCTTCTGCGCTGGGTGGCAGATTAACGACTGCTCTTCAAAATAC 21694
QY 781 ATGCACAAAAAGTACCGCACAAGCAAAACACCGAGGAATTTCATATAGACAGAGGGTGAC 840
DB 21695 ATGCACAAAAAGTACCGCACAAGCAAAACACCGAGGAATTTCATATAGACAGAGGGTGAC 21754
QY 841 CACCCCTAAGGCGATTGATGATGGAGGAATGATGTAATCCCATTTTCTAGATGGGAAC 900
DB 21755 CACCCCTAAGGCGATTGATGATGGAGGAATGATGTAATCCCATTTTCTAGATGGGAAC 21814
QY 901 CTGGTGCCCTCGAAGGGAAGAAAGTGAATGATCCCGCAGAGATGATCCGATTTCTC 960
DB 21815 CTGGTGCCCTCGAAGGGAAGAAAGTGAATGATCCCGCAGAGATGATCCGATTTCTC 21874
QY 961 AAGGATCTGAAGCAAAAACCCAGAGAGAGGACTTATGATGATGATGGAGTGGCCAAAT 1020
DB 21875 AAGGATCTGAAGCAAAAACCCAGAGAGAGGACTTATGATGATGATGGAGTGGCCAAAT 21934
QY 1021 TACTATGCTCTTCCCAACCAAGAAAGAGCGCGCTTACCGTATCCAAAGCAGCTGCT 1080
DB 21935 TACTATGCTCTTCCCAACCAAGAAAGAGCGCGCTTACCGTATCCAAAGCAGCTGCT 21994
QY 1081 ATGATGACTGTGTCAGGCAATATCTGMAAAGAAACATGACAGACAAAGCAAGAAAGGCC 1140
DB 21995 ATGATGACTGTGTCAGGCAATATCTGMAAAGAAACATGACAGACAAAGCAAGAAAGGCC 22054
QY 1141 TCCAGATGAGCGAGGTCGACACGAGTACGAGGAGGCTTATTTCCAAAGGCTCTCTTT 1200
DB 22055 TCCAGATGAGCGAGGTCGACACGAGTACGAGGAGGCTTATTTCCAAAGGCTCTCTTT 22114
QY 1201 GACCCATGTTCTTACCACTCTGAGAACTGTGGGGCTTACTCTGACAGTGGTGAGG 1260
DB 22115 GACCCATGTTCTTACCACTCTGAGAACTGTGGGGCTTACTCTGACAGTGGTGAGG 22174
QY 1261 AAAAGGGGAGCATGTCAAAAGCAATGTATGTGACTACAAAACAGAGATGGTCTGCC 1320
DB 22175 AAAAGGGGAGCATGTCAAAAGCAATGTATGTGACTACAAAACAGAGATGGTCTGCC 22234
QY 1321 AATGCAAGGGCTGACATATAGTTTACAGAGGAGCAGGCTGTCTGAAAGCCAGAGAGAGCC 1380
DB 22235 AATGCAAGGGCTGACATATAGTTTACAGAGGAGCAGGCTGTCTGAAAGCCAGAGAGAGCC 22294
QY 1381 CAGAGAGATTTCCGAGGCGCATTAATTGATGACACATTTTGTAGAGAGATGAACCTTC 1440
DB 22295 CAGAGAGATTTCCGAGGCGCATTAATTGATGACACATTTTGTAGAGAGATGAACCTTC 22354
QY 1441 TTTGTAAAGTTGAACATGTCCGATATAGAGAGAGACAGCAGAGAGAGGAGTGCCTCCA 1500
DB 22355 TTTGTAAAGTTGAACATGTCCGATATAGAGAGAGACAGCAGAGAGAGGAGTGCCTCCA 22414
QY 1501 GCAATATTTCAACAGTCTTCCCTTGGCTCGGGGCTGTCTAGACCTCCCTTGTGTGGCCACA 1560
DB 22415 GCAATATTTCAACAGTCTTCCCTTGGCTCGGGGCTGTCTAGACCTCCCTTGTGTGGCCACA 22474
QY 1561 GTTACCATCTTGGATGATGACATGACAGGAGCATTTCACTTTGAAATGTGATTAATTCAAT 1620
DB 22475 GTTACCATCTTGGATGATGACATGACAGGAGCATTTCACTTTGAAATGTGATTAATTCAAT 22534

Qy 1621 GTCAGTACAGTATGTTGTTATGAGAGTCAAGTTCGCGACATCAGTCCCGGGGT 1680
|||||
Db 22535 GTCAGTACAGTATGTTGTTATGAGAGTCAAGTTCGCGACATCAGTCCCGGGGT 22594
Qy 1681 ACAGTCATCGTCCCTTTAGACAGTAGAGGACGCCAAGGTCGGGTGAGACTTT 1740
|||||
Db 22595 ACAGTCATCGTCCCTTTAGACAGTAGAGGACGCCAAGGTCGGGTGAGACTTT 22654
Qy 1741 GAAGACATATGGGGAGTTGGAATTCGAATGTAAGTGAAGTGA 1788
|||||
Db 22655 GAAGACATATGGGGAGTTGGAATTCGAATGTAAGTGAAGTGA 22702
RESULT 11
AC009607
LOCUS AC009607 146055 bp DNA linear HTG 04-MAY-2001
DEFINITION Homo sapiens clone Rpl1-1111, WORKING DRAFT SEQUENCE, 31 unordered
pieces.
AC009607 GI:8072446
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Ctenolata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 146055)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone Rpl1-1111
Unpublished
2 (bases 1 to 146055)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dattrelano,K., Depayre,E., Devon,K., Dewar,K.,
Donelan,J., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
Karatas,A., Lehoczy,J., Liu,C., Locke,K., Macdonald,P.,
Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
Meidlor,J., Moll,M., Morris,W., Morrow,J., Mychaleckyj,J.,
Naylor,J., Nilotoff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
Tefaye,S., Toruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
Wheeler,O., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
Direct Submission
Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced gi:7321520.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Smit,A.F.A. & Green,P. (1996-1997)
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
----- Project Information
Center project name: L1464
Center clone name: 1_111
----- Summary Statistics
Sequencing vector: M13; M77815; 99% of reads
Sequencing method: Plasmid; n/a; 8-0.1% of reads
Chemistry: Dye-terminator Big Dye; 94% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 126247 bases at least Q40
Consensus quality: 134710 bases at least Q30
Insert size: 160000; agarose-ef
Insert size: 143055; sum-of-ctrls
Quality coverage.
* NOTE: This is a 'working draft' sequence. It currently

FEATURES
Source
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1166: contig of 1166 bp in length
1167 1266: gap of 100 bp
1267 2417: contig of 1151 bp in length
2418 2517: gap of 100 bp
2518 3635: contig of 1118 bp in length
3636 3735: gap of 100 bp
3736 4851: contig of 1116 bp in length
4852 4951: gap of 100 bp
4952 6701: contig of 1750 bp in length
6702 6801: gap of 100 bp
6802 8629: contig of 1828 bp in length
8630 8729: gap of 100 bp
8730 10482: contig of 1753 bp in length
10483 10582: gap of 100 bp
10583 12126: contig of 1544 bp in length
12127 12226: gap of 100 bp
12227 13831: contig of 1605 bp in length
13832 13931: gap of 100 bp
13932 16132: contig of 2201 bp in length
16133 16232: gap of 100 bp
16233 17951: contig of 1719 bp in length
17952 18051: gap of 100 bp
18052 20069: contig of 2018 bp in length
20070 20169: gap of 100 bp
20170 22565: contig of 2296 bp in length
22566 22665: gap of 100 bp
22666 24924: contig of 2259 bp in length
24925 25024: gap of 100 bp
25025 26996: contig of 1972 bp in length
26997 27096: gap of 100 bp
27097 28834: contig of 1738 bp in length
28835 28934: gap of 100 bp
28935 33803: contig of 4869 bp in length
33804 33903: gap of 100 bp
33904 38177: contig of 4274 bp in length
38178 38277: gap of 100 bp
38278 42132: contig of 3855 bp in length
42133 42232: gap of 100 bp
42233 45874: contig of 3642 bp in length
45875 45974: gap of 100 bp
45975 50807: contig of 4833 bp in length
50808 50907: gap of 100 bp
50909 55690: contig of 4783 bp in length
55691 55790: gap of 100 bp
55791 60868: contig of 5078 bp in length
60869 60968: gap of 100 bp
60969 65180: contig of 4212 bp in length
65181 65280: gap of 100 bp
65281 72495: contig of 7215 bp in length
72496 72595: gap of 100 bp
72596 79536: contig of 6941 bp in length
79537 79636: gap of 100 bp
79637 86013: contig of 6377 bp in length
86014 86113: gap of 100 bp
86114 98467: contig of 12354 bp in length
98468 98567: gap of 100 bp
98568 112312: contig of 13745 bp in length
112313 112412: gap of 100 bp
112413 128733: contig of 16321 bp in length
128734 128833: gap of 100 bp
128834 146055: contig of 17222 bp in length.
Location/Qualifiers
1. 146055
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Rpl1-1111"

misc_feature	/clone_11b-"RPOI-11 Human Male BAC"
misc_feature	1..1166
misc_feature	/note="assembly_fragment"
misc_feature	1267..2417
misc_feature	/note="assembly_fragment"
misc_feature	2518..3635
misc_feature	/note="assembly_fragment"
misc_feature	3736..4851
misc_feature	/note="assembly_fragment"
misc_feature	4952..6701
misc_feature	/note="assembly_fragment"
misc_feature	6802..8629
misc_feature	/note="assembly_fragment"
misc_feature	8730..10482
misc_feature	/note="assembly_fragment"
misc_feature	10583..12126
misc_feature	/note="assembly_fragment"
misc_feature	12227..13831
misc_feature	/note="assembly_fragment"
misc_feature	13932..16132
misc_feature	/note="assembly_fragment"
misc_feature	16233..17951
misc_feature	/note="assembly_fragment"
misc_feature	18052..20069
misc_feature	/note="assembly_fragment"
misc_feature	20170..22565
misc_feature	/note="assembly_fragment"
misc_feature	22666..24924
misc_feature	/note="assembly_fragment"
misc_feature	25025..26996
misc_feature	/note="assembly_fragment"
misc_feature	27097..28834
misc_feature	/note="assembly_fragment"
misc_feature	clone_end:SP6
misc_feature	vector_side:left"
misc_feature	28935..33803
misc_feature	/note="assembly_fragment"
misc_feature	33904..38177
misc_feature	/note="assembly_fragment"
misc_feature	38278..42132
misc_feature	/note="assembly_fragment"
misc_feature	42233..45874
misc_feature	/note="assembly_fragment"
misc_feature	clone_end:T7
misc_feature	vector_side:left"
misc_feature	45975..50807
misc_feature	/note="assembly_fragment"
misc_feature	50908..55690
misc_feature	/note="assembly_fragment"
misc_feature	55791..60868
misc_feature	/note="assembly_fragment"
misc_feature	60969..65180
misc_feature	/note="assembly_fragment"
misc_feature	65281..72495
misc_feature	/note="assembly_fragment"
misc_feature	72596..79536
misc_feature	/note="assembly_fragment"
misc_feature	79637..86013
misc_feature	/note="assembly_fragment"
misc_feature	86114..98467
misc_feature	/note="assembly_fragment"
misc_feature	98568..112312
misc_feature	/note="assembly_fragment"
misc_feature	112413..128733
misc_feature	/note="assembly_fragment"
misc_feature	128834..146055
misc_feature	/note="assembly_fragment"
BASE COUNT	41047 a 30113 c 30523 g 41366 t 3006 others
ORIGIN	
Query Match	64.5%: Score 1784.8; DB 2; Length 146055;
Best Local Similarity	99.9%: Pred.No. 0;
Matches 1786: Conservative	0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGGGTGGTTAAAGTTGTCACACCTCTCAACCTCCGCTTCCATTTTGGGGTGGTTACC	60
Db	138575	ATGGGTGGTTAAAGTTGTCACACCTCTCAACCTCTCTCTCCATTTTGGGGTGGTTACC	138634
QY	61	TTTGTGCTCTTCCTGAAATGATCTTTCGAGCAGAGGCTGGTGGCTCAGGGAGCTGCCAAGC	120
Db	138635	TTTGTGCTCTTCCTGAAATGATCTTTCGAGCAGAGGCTGGTGGCTCAGGGAGCTGCCAAGC	138694
QY	121	ACAGGGCAGAAACAATGAACTCTCTGTTCAAGGTCATCCGACATCTGCAAGAGGGGTGCATCTCG	180
Db	138695	ACAGGGCAGAAACAATGAACTCTCTGTTCAAGGTCATCCGACATCTGCAAGAGGGGTGCATCTCG	138754
QY	181	CCAAATCTGATACCCGAGAAACCCCTTCCCTTTGGGGACAAGATTTGCCAGGCTCATTTGCTAT	240
Db	138755	CCAAATCTGATACCCGAGAAACCCCTTCCCTTTGGGGACAAGATTTGCCAGGCTCATTTGCTAT	138814
QY	241	TTTTGTGCCCCCTGATATACATGTTCTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	300
Db	138815	TTTTGTGCCCCCTGATATACATGTTCTCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA	138874
QY	301	TCTATTGAAGTCATACCTCTCAAGAGAGGGAGGTGCATTTAAGAAACCATAGGAGAA	360
Db	138875	TCTATTGAAGTCATACCTCTCAAGAGAGGGAGGTGCATTTAAGAAACCATAGGAGAA	138934
QY	361	ACCAGCACAAACCACTATTGCGGGTCTGGAATGAAACTGTCTCCAACTGCACCTTATGGCC	420
Db	138935	ACCAGCACAAACCACTATTGCGGGTCTGGAATGAAACTGTCTCCAACTGCACCTTATGGCC	138994
QY	421	CTGGGTTCTCTGCTGCCCGCAGATACCTCTCTTAAATTAAGGTGTGGTTCATAGGGTTTC	480
Db	138995	CTGGGTTCTCTGCTGCCCGCAGATACCTCTCTTAAATTAAGGTGTGGTTCATAGGGTTTC	139054
QY	481	ATTGCTGTGATCTGGGACCTTCTACCAATGTTAGGGAGTGCAGCCTTCAACATGTTTCATC	540
Db	139055	ATTGCTGTGATCTGGGACCTTCTACCAATGTTAGGGAGTGCAGCCTTCAACATGTTTCATC	139114
QY	541	ATCATTTGGCATCTGTGTACTGTAATCCACAGGAGAGACTGGCAAGATCAAGCATCTA	600
Db	139115	ATCATTTGGCATCTGTGTACTGTAATCCACAGGAGAGACTGGCAAGATCAAGCATCTA	139174
QY	601	CGAGCTCTTCTTCAATACACGCTGCTTGGAGATCTTTGCCATCATCTGGCTCTATATGATT	660
Db	139175	CGAGCTCTTCTTCAATACACGCTGCTTGGAGATCTTTGCCATCATCTGGCTCTATATGATT	139234
QY	661	CTGGCAGTCTTCTCCCTGATGTGTGTCCAGGTTTGGAGAGGCTCTCACTCTCTTCTTC	720
Db	139235	CTGGCAGTCTTCTCCCTGATGTGTGTCCAGGTTTGGAGAGGCTCTCACTCTCTTCTTC	139294
QY	721	TTTCCAGTGTGTGTCTTCTGGCTGGGGTGGCAATPAAGAGCTGCTCTTCAAAATAC	780
Db	139295	TTTCCAGTGTGTGTCTTCTGGCTGGGGTGGCAATPAAGAGCTGCTCTTCTCAAAATAC	139354
QY	781	ATGCACAAAAGATACCGCACAGACAAACACCGAGAGATTATCATAGACAGAGGGTGAC	840
Db	139355	ATGCACAAAAGATACCGCACAGACAAACACCGAGAGATTATCATAGACAGAGGGTGAC	139414
QY	841	CACCTTAAGGGCATTTAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAC	900
Db	139415	CACCTTAAGGGCATTTAGATGGATGGGAAAATGATGAATTCCTATTTCTAGATGGGAC	139474
QY	901	CTGGGTGCCCTTGGAAAGGAAGATGGATAGTCCCGCAGAGAGATGATCCGGATTCTC	960
Db	139475	CTGGGTGCCCTTGGAAAGGAAGATGGATAGTCCCGCAGAGAGATGATCCGGATTCTC	139534
QY	961	AAGGATCTGAAGCAAAAAACACCCAGAGAAAGCACTTAGATCAGCTGTGTGAGATGGCCAAAT	1020
Db	139535	AAGGATCTGAAGCAAAAAACACCCAGAGAAAGCACTTAGATCAGCTGTGTGAGATGGCCAAAT	139594
QY	1021	TACTATGCTCTTTTCCCAACAACAAGAGCCGCCCTTCTACCGGTATCCAAAGCCACTCGT	1080
Db	139595	TACTATGCTCTTTTCCCAACAACAAGAGCCGCCCTTCTACCGGTATCCAAAGCCACTCGT	139654

OY 1081 ATGATGACTGTGACGACATATCTGAGAAAAATGACGACAAACCAAGAGGCC 1140
 |||||||
 DB 139655 ATGATGACTGTGACGACATATCTGAGAAAAATGACGACAAACCAAGAGGCC 139714
 |||||||
 OY 1141 TCCAGCATGAGGAGGTGACACACCCGATGAGCCTTATATTTCAAGGCTCTCTTT 1200
 |||||||
 DB 139715 TCCAGCATGAGGAGGTGACACACCCGATGAGCCTTATATTTCAAGGCTCTCTTT 139774
 |||||||
 OY 1201 GACCCATGTTTACACAGTCCGAGAACTGTGGGCTGTACTCTGTACAGTGGTGGAG 1260
 |||||||
 DB 139775 GACCCATGTTTACACAGTCCGAGAACTGTGGGCTGTACTCTGTACAGTGGTGGAG 139834
 |||||||
 OY 1261 AAAGGGGAGACATGTCACAGACCATGTATGTGACTACAAAACAGAGATGTTTGGC 1320
 |||||||
 DB 139835 AAAGGGGAGACATGTCACAGACCATGTATGTGACTACAAAACAGAGATGTTTGGC 139894
 |||||||
 OY 1321 AATGCGGGGCTGACTATGATGACAGAGGCGACGGTCTTGAAGCCAGAGAGACC 1380
 |||||||
 DB 139895 AATGCGGGGCTGACTATGATGACAGAGGCGACGGTCTTGAAGCCAGAGAGACC 139954
 |||||||
 OY 1381 CAGAGAGATGTTCCCTGGGCAATATTTGATGACGACATTTTGGAGAGATGAACCTTC 1440
 |||||||
 DB 139955 CAGAGAGATGTTCCCTGGGCAATATTTGATGACGACATTTTGGAGAGATGAACCTTC 140014
 |||||||
 OY 1441 TTTGTAAAGTTGAGCAATGTCCGATAGAGAGACAGACAGAGAGGAGATGCTCCA 1500
 |||||||
 DB 140015 TTTGTAAAGTTGAGCAATGTCCGATAGAGAGACAGACAGAGAGGAGATGCTCCA 140074
 |||||||
 OY 1501 GCAATATTCACAGTCTTCCCTGCGGCTGTCTAGCCCTCCCTTGTGTGGCCACA 1560
 |||||||
 DB 140075 GCAATATTCACAGTCTTCCCTGCGGCTGTCTAGCCCTCCCTTGTGTGGCCACA 140134
 |||||||
 OY 1561 GTTACCATCTGGATGATGATGACCATGACGACATCTTCAATTTGAATGATATTCAT 1620
 |||||||
 DB 140135 GTTACCATCTGGATGATGATGACCATGACGACATCTTCAATTTGAATGATATTCAT 140194
 |||||||
 OY 1621 GTGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 |||||||
 DB 140195 GTGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 140254
 |||||||
 OY 1681 ACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 |||||||
 DB 140255 ACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 140314
 |||||||
 OY 1741 GAAGACACATATGAGGAGTGGATGATGATGATGATGATGATGATGATGATGAT 1788
 |||||||
 DB 140315 GAAGACACATATGAGGAGTGGATGATGATGATGATGATGATGATGATGATGAT 140362
 |||||||

RESULT 12
 CENSORING 206256 bp DNA 1linear PRI 10-JUL-2001
 LOCUS Human chromosome 14 DNA sequence BAC R-486013 of library RPI-11
 DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
 ACCESSION AL160191.3 GI:14715172
 VERSION 1
 KEYWORDS HTG: HTGS_ACTIVEFIN.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 206256)
 HELIG, R., PETIT, J.L., VICO, V., DASILVA, C., ROBERT, C., WINCKER, P.,
 BROTTIER, P., CATOLICO, L., BAIRE, V., PELLETIER, E., ARTIGUENAVE, F.,
 LEVY, M., ECKENBERG, R., BRUNS, T., DEBERARDINIS, V., CRUAUD, C.,
 GYAPAY, G., SAUTIN, W. and WEISENBACH, J.
 Sequencing of the human chromosome 14
 Unpublished
 2 (bases 1 to 206256)
 Genoscope.
 Direct Submission
 Submitted (09-JUL-2001) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)

COMMENT
 - Web : www.genoscope.cns.fr
 On Jul 12, 2001 this sequence version replaced gi:7708226.
 ----- Genome Center
 Center: Genoscope / Centre National de Sequencage
 Center code: GS
 Web site: <http://www.genoscope.cns.fr/>
 Contact: Segref@genoscope.cns.fr

 The following BAC sequence is oriented from the T7 to the SP6 end.
 Upstream BAC (overlapping the T7 end) : R-71862 (AC-AL356804)
 Downstream BAC (overlapping the SP6 end) : R-1023122
 ----- Summary Statistics
 Assembly program: Phrap; version 2.0
 Quality coverage: 8.36x in Q20 bases; sum-of-contigs

 Overall quality chart :
 Range : bases
 0 :
 1 - 9 : 7
 10 - 19 : 78
 20 - 29 : 197
 30 - 39 : 1106
 40 - 49 : 5627
 50 - 59 : 11755
 60 - 69 : 10932
 70 - 79 : 18529
 80 - 89 : 46808
 90 - 99 : 111227

 Percentage of bases with a quality value >= 40 : 99 %.

 FEATURES
 source
 1.206256
 location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="14"
 /clone="R-486013"
 /clone_1lb="RPI-11"
 /length="16970"
 /note="matching EMBL:AF029900
 RHD:RH103433
 dbSTS:STS70962
 identified using the e-PCR software (G. Schuler)"
 72147..72239
 /note="matching EMBL:G37613
 RHD:RH101557
 RHD:RH82090
 dbSTS:STS58442
 identified using the e-PCR software (G. Schuler)"
 116803..116967
 /note="matching EMBL:Z44310
 RHD:RH26997
 dbSTS:STS15075
 identified using the e-PCR software (G. Schuler)"
 118337..118551
 /note="matching EMBL:Z38712
 RHD:RH10057
 dbSTS:STS12967
 identified using the e-PCR software (G. Schuler)"
 144730..144853
 /note="matching EMBL:F13424
 RHD:RH44806
 dbSTS:STS37874
 identified using the e-PCR software (G. Schuler)"
 145994..146150
 /note="matching EMBL:F17195
 RHD:RH78238
 dbSTS:STS54980
 identified using the e-PCR software (G. Schuler)"
 146051..146200
 /note="matching EMBL:HI5034
 RHD:RH53547
 dbSTS:STS14940

STS	Identified using the e-PCR software (G. Schuler)"
147348 . 147523	/note="matching EMBL: Z23692
RHdb: RH9565	
dbSTS: SFS25409	
Identified using the e-PCR software (G. Schuler)"	
147371 . 147522	/note="matching EMBL: Z23692
RHdb: RH73223	
RHdb: RH49065	
RHdb: RH13015	
RHdb: RH376	
dbSTS: SFS30523	
Identified using the e-PCR software (G. Schuler)"	
59769 a 43632 c 43686 g 59169 t	

SEQUENCE, 14 unordered pieces.

ACCESSION AC124384

VERSION AC124384.2 GI:21702965

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 186831)

AUTHORS McPherson, J.D. and Waterston, R.H.

TITLE The sequence of Mus musculus clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 186831)

AUTHORS McPherson, J.D. and Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 3 (bases 1 to 186831)

AUTHORS McPherson, J.D. and Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (07-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Jul 7, 2002 this sequence version replaced gi:21426504.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

Contact: submissions@watson.wustl.edu

----- Project Information -----

Center project name: M_BB0413602

----- Summary Statistics -----

Sequencing vector: M13; 0%

Sequencing vector: plasmid; 100%

Chemistry: Dye-primer ET; 0% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 180539 bases at least Q40

Consensus quality: 181771 bases at least Q30

Consensus quality: 182641 bases at least Q20

Insert size: 184000; agarose-1p

Insert size: 185531; sum-of-ctrls

Quality coverage: 10.38 in Q20 bases; agarose-1p

Quality coverage: 9.64 in Q20 bases; sum-of-ctrls

----- NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. -----

1 1407: contig of 1407 bp in length

* 1408 1507: gap of unknown length

* 1508 2752: contig of 1245 bp in length

* 2753 2852: gap of unknown length

* 2853 4166: contig of 1314 bp in length

* 4167 4267: gap of unknown length

* 4267 5895: contig of 1629 bp in length

* 5896 5995: gap of unknown length

* 5996 13670: contig of 7675 bp in length

* 13671 13770: gap of unknown length

* 13771 21208: contig of 7438 bp in length

* 21209 21308: gap of unknown length

* 21309 30054: contig of 8746 bp in length

* 30055 30154: gap of unknown length

* 30155 38422: contig of 8268 bp in length

* 38423 38522: gap of unknown length

* 38523 55197: contig of 16575 bp in length

* 55198 55197: gap of unknown length

* 55198 76384: contig of 21187 bp in length

FEATURES

SOURCE

1. 186831

/organism="Mus musculus"

/db_xref="taxon:10090"

/chromosome="UNK"

/clone="RP24-41362"

1. 1407

/note="assembly_name:Contig26"

1508. .2752

/note="assembly_name:Contig28"

2853. .4166

/note="assembly_name:Contig34"

4267. .5895

/note="assembly_name:Contig36"

5996. .13670

/note="assembly_name:Contig37

clone_end:r7

vector_side:right"

13771. .21208

/note="assembly_name:Contig38

clone_end:SP6

vector_side:left"

21309. .30054

/note="assembly_name:Contig39"

30155. .38422

/note="assembly_name:Contig40"

38523. .55097

/note="assembly_name:Contig41"

55198. .76384

/note="assembly_name:Contig42"

76485. .96442

/note="assembly_name:Contig43"

96543. .117119

/note="assembly_name:Contig44"

117220. .154744

/note="assembly_name:Contig45"

154845. .186831

/note="assembly_name:Contig46"

BASE COUNT 51956 a 41497 c 40299 g 51731 t 1348 others

ORIGIN

Query Match 55.9%; Score 1546.4; DB 2; Length 186831;

Best Local Similarity 91.6%; Pred. No. 0;

Matches 1637; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

1 ATGGCGTGGTAAAGTTGAGCGCTCAGCTTCACCTTCCTCCATTTGGCGTACC 60

||||| 11 |||||||

DB 112636 ATGGCGTGGTAAAGTTGAGCGCTCAGCTTCACCTTCCTCCATTTGGCGTACC 112695

61 TTTGTGCTCTTCCTGAATGCTTCGAGCAGAGCGTGTGCTCAGAGGAGCGTCCAGC 120

||||| 11 |||||||

DB 112696 TTTGTGCTCTTCCTGAATGCTTCGAGCAGAGCGTGTGCTCAGAGGAGCGTCCAGC 112755

121 ACAGGCAACAACAAATGAGTCTGTTACAGGCTATCGAGATCGCAAGAGAGGCTCATCCG 180

||||| 11 |||||||

DB 112756 GAGGGCAACAACAAATGAGTCTGTTACAGGCTATCGAGATCGCAAGAGAGGCTCATCCG 112815

181 CCAATCTGTACCCGAGAACCTTCCTGGGAGCAAGATTCAGAGGCTCATTTGCTAT 240

||||| 11 |||||||

DB 112816 CCAATCTGTATCCAGAGAACCTTCCTGGGAGCAAGATTCAGAGGCTCATTTGCTAT 112875

241 TTTGTGCGCCCTGATATATATGTTCTTGGGGTGTCCATTCATTCGACCGCTTCATGCA 300

||||| 11 |||||||

DB 112876 TTTGTGCGCCCTGATATATATGTTCTTGGGGTGTCCATTCATTCGACCGCTTCATGCA 112935

QY 301 TCTATTGAGTCATACCTCTCAAGAGAGGAGTGACAAATTAGAAAACCAATGAGAA 360
|||||
Db 112936 TCTATTGAGTCATACCTCTCAAGAGAGGAGTGACAAATTAGAAAACCAATGAGAG 112995
QY 361 ACCGACACACCACTATTCGGGCTGGAGATGAACCTGTCTCAACCTGACCTTATGGCC 420
|||||
Db 112996 ACCGACACACCACTATTCGGGCTGGAGATGAACCTGTCTCAACCTGACCTTATGGCC 113055
QY 421 CTGGGCTCTCTGCTCCGAGATCTCTCTTAATGAGATGGTGGATGGATTC 480
|||||
Db 113056 CTGGGCTCTCTGCTCCGAGATCTCTCTTAATGAGATGGTGGATGGATTC 113115
QY 481 ATTGCTGTGATCTGGAGACCTTCTACCATTTAGAGAGTGAGACCTTCAACATGTTATC 540
|||||
Db 113116 ATTGCTGTGATCTGGAGACCTTCTACCATTTAGAGAGTGAGACCTTCAACATGTTATC 113175
QY 541 ATCATTTGGCATCTGTCTACGTATGATCCAGACGAGAGACTGCCAAGATCAACATCTA 600
|||||
Db 113176 ATCATTTGGCATCTGTCTACGTATGATCCAGATGGGAGACTGCCAAGATCAACACCTG 113235
QY 601 CGAGTCTCTCTCATCACCGCTGTTGGAGATCTTTGGCTCATCTGGCTATATGATT 660
|||||
Db 113236 CGAGTCTCTCTCATCACCGCTGTTGGAGATCTTTGGCTCATCTGGCTATATGATT 113295
QY 661 CTGGCAGTCTCTCTCCCTGT 720
|||||
Db 113296 CTGGCAGTCTCTCTCCCTGT 113355
QY 721 TTTCCATGTGTCT 780
|||||
Db 113356 TTTCCATGTGTCT 113415
QY 781 ATGCACAAAAAGTACCGACAGACACACACCGAGAAATTTATCATAGAGACAGAGGTTGAC 840
|||||
Db 113416 ATGCACAAAAAGTACCGACAGACACACACCGAGAAATTTATCATAGAGACAGAGGTTGAC 113475
QY 841 CACCTTAAGGGCATTTAGATGATGGGAAAAATGATGATTTCCATTTCTAGATGGGAAAC 900
|||||
Db 113476 CACCTTAAGGGCATTTAGATGATGGGAAAAATGATGATTTCTCATTTCTAGATGGGAAAC 113535
QY 901 CTGGTGGCCCTGGAGAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
|||||
Db 113536 TTTACACCTTTGGAGAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 113595
QY 961 AAGGATCTGAAGCAAAAAACACCCAGAGAGGACTTATGATGATGATGATGATGATGATGAT 1020
|||||
Db 113596 AAGGATCTGAAGCAAAAAACACCCAGAGAGGACTTATGATGATGATGATGATGATGATGAT 113655
QY 1021 TACTATGCTCTTTCCACCAACAGAGAGGCGGCTTCTTACCGTATTCAGAGCACTGCT 1080
|||||
Db 113656 TACTATGCTCTTTCCACCAACAGAGAGGCGGCTTCTTACCGTATTCAGAGCACTGCT 113715
QY 1081 ATGATGATCTGTGAGGCAAAATCTCTGAAGAAATGATGATGATGATGATGATGATGATGAT 1140
|||||
Db 113716 ATGATGATCTGTGAGGCAAAATCTCTGAAGAAATGATGATGATGATGATGATGATGATGAT 113775
QY 1141 TCCAGCATGAGACGAGTGACACAGCATGAGCTTATGATGATGATGATGATGATGATGATGAT 1200
|||||
Db 113776 TCCAGCATGAGACGAGTGACACAGCATGAGCTTATGATGATGATGATGATGATGATGATGAT 113835
QY 1201 GACCCATGTTCTTACAGAGTGCGTGGAGAACTGTGGGCTGTACTCTGACAGTGTGAGG 1260
|||||
Db 113836 GACCCATGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 113895
QY 1261 AAAGGGGAGCATGTCTCAAGACCATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
|||||
Db 113896 AAAGGGGAGCATGTCTCAAGACCATGATGATGATGATGATGATGATGATGATGATGATGAT 113955
QY 1321 AATCAGAGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
|||||
Db 113956 AATCAGAGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 114015
QY 1381 CAGAAGAGATTCTCCGTGGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

Db 114016 CAGAAGAGATTCTCCGTGGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 114075
QY 1441 TTTGAT 1500
|||||
Db 114076 TTTGAT 114135
QY 1501 GCAATATTTCAACAGCT 1560
|||||
Db 114136 GCAATATTTCAACAGCT 114195
QY 1561 GTTACATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
|||||
Db 114196 GTTACATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 114255
QY 1621 GTTACATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
|||||
Db 114256 GTTACATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 114315
QY 1681 ACACTCATGCT 1740
|||||
Db 114316 ACACTCATGCT 114375
QY 1741 GAAGACACATATGAGGAGGAGTTGAAATTCAGAGATGATGATGATGATGATGATGATGATGAT 1788
|||||
Db 114376 GAAGACACATATGAGGAGGAGTTGAAATTCAGAGATGATGATGATGATGATGATGATGATGAT 114423
RESULT 14
AF321404
LOCUS AF321404 1784 bp mRNA linear ROD 06-MAR-2001
DEFINITION Mus musculus sodium-calcium exchanger 3 (Slc8a3) mRNA, partial cds.
ACCESSION AF321404
VERSION AF321404.2 GI:133236894
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 1784)
Sokolow,S., Hercheulz,A. and Schurmans,S.
TITLE Mus musculus mRNA for sodium-calcium exchanger 3 (NCX3), partial
sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1784)
Sokolow,S., Hercheulz,A. and Schurmans,S.
AUTHORS Direct Submission
TITLE Submitted (14-NOV-2000) I.R.B.N., Free University of Brussels,
JOURNAL rue A Bolland, Gosselies 6041, Belgium
COMMENT On Mar 6, 2001 this sequence version replaced gi:11993637.
FEATURES
source
1..1784
location/Qualifiers
1..1784
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="12"
1..>1784
/gene="Slc8a3"
/note="NCX3"
1..>1784
/gene="Slc8a3"
/note="NCX3"
/note="NCX3; exon 2"
/product="sodium-calcium exchanger 3"
/protein_id="AAG42826.2"
/db_xref="GI:133236895"
/translation="MAMLRDPLTSAFLHGLVTVFLNCLRAEAGDSGDVPSAGQ
NESGSSSDCKEIVLPWPENPISLGDIKARIYVFAVLIYFLGVSIADPFMSI
EYTSQREVTIKRPNGESTSTIRVMNEVSNLTLALGSSAPETLLSILIEVGHGF
IAGDLSPSTVIGSAARNMFLIIGICVYIPDGETRIKHLRVEFVAAMSIFAYIMLY
MTLAVSPGVQYWEGLTLPFRPNCVILLAMVDKRLFLFYKNNKKYRPDKHNGITTE
TEGDHFKGEMDKMNSHFLDGNFTPLBEKYEDESREMRIRLKLKOKHPEKDIDQ
LVEMANVIALSHOQSRATFYRIQATRMNMGAGNIIKHADEAKKTSMSSEVHTDPE
DFASKVFFPCSYQCLENCGAVLLTVVRGGDISKTMVYDKTEGDSANAGADYEFE

JOURNAL J. Endocrinol. 168 (3), 517-526 (2001)
MEDLINE 21136211
PUBMED 11241183
REFERENCE 2 (bases 1 to 2814)
AUTHORS Van Eylen, F., Bollen, A. and Herchuelz, A.
TITLE Direct Submission
JOURNAL Submitted (23-NOV-1998) Pharmacodynamic, Brussels Free University,
Route de Lemik 808, C.P. 617, Brussels 1070, Belgium
FEATURES
source
1. .2814
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1. .2814
/gene="NCX1"
1. .2814
/note="NCX1"
/note="isoform NCX1.3"
/codon_start=1
/product="sodium/calcium exchanger isoform NaCa3"
/protein_id="AF08988.1"
/db_xref="GI:6453729"
/translation="MYNMRSLSPFNSMFLVTVSILFSDVHVIATFEMEGSN
ETRECGSYCKKGVILPIREFPODPSFGDKIATATYFVAMVYMFPGVSTIARPHSS
IEVTSOEKITIKKPNGETTKTVRIWNTVSNLTLMALGSAPELILSVIECGHN
FTAGDLGPSTIVGSAFNMFIILALCVVPAVDGTRIKRLRVFVTAASIFAATWL
YILSVISPGVVEWEGELFFEPFLCVVPAVDGTRIKRLRVFVTAASIFAATWL
EHGDRPSKTEIEMDGKVNSENHENDLALVLEVERDODEEARREMARILKEIK
OKHDKIEQLILANVOVLSOOKSRAPIRIOTATIRGSGULTVIVPDRFBEGT
MHEVNEVTPNDPVSKIFEEQGYOCLENGCTVALTIRRGSGULTVIVPDRFBEGT
ANGSDIEFEGTVKVERPDQKELRIGLIDDDIFEDENFLVLSVWKSSEASDQ
ILBANVSTLACGSPSTATVIFDDHAIFFEEVNVHSSISIGMEVKLRTSQA
RGNVIVPKTIEGTARGGDEPDGTEGELFONDEIVKITTIRIPREVEKESFSL
VLEPEKMRIRMGCGFTITDEYDKOPLTEKEERIRIAGMRPIIGENHKLVLIEE
SYEFSKTVDLIKKTNLALVYGNSEORIEATVYAGSDDDDEGEKLEPCDY
VMHLYVEKVLFAFVPRPYNMGACFIYSIIMIGLTFIDLSAHSRECTGLDLS
VTAIVFVALCTSVPTDFASRVKATODQADASIGNVTGSAVAVFLIGIYAMSLAII
HAANGDFKVSPTGLAFSVLTFTIFAFINVGILYRRRPEIGGELGPPRYAKLITSL
FVLLMLYIFSSILEAVYCHIKGF"

BASE COUNT 754 a 579 c 718 g 763 t
ORIGIN

Query Match 48.08; Score 1326.4; DB 9; Length 2814;
Best Local Similarity 69.86; Pred. No. 1,4e-313;
Matches 1893; Conservative 0; Mismatches 756; Indels 63; Gaps 5;

109 GACGTGCCAACGACGAGGACAGACATGAGTCTGTTCAGGCTATCGAGCTGCAGAGAG 168
112 GAATGAGAGAGAGAGAAATGAAATGCTGATCTGATCATATATCTATTGTAAGAAA 171
169 GGTGTCAATCTGCAATCTGGTACCCGAGAAACCTTCCCTTGGGACAGATTGCCAGG 228
172 GGGGTGATTTTGGCCATTTGGGAAACCCCAACCTTCTTTGGGACAAATGCTAGA 231
229 GTCAATGCTATTTTGGGCCCCGATATACATGTTCTTGGGGGTGCTCATATGCTGAC 288
232 GCTACTGATGATTTTGGGCCCCGATATACATGTTCTTGGGGGTGCTCATATGCTGAT 291
289 CGCTTCATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 348
292 CGGTTCATGCTCTATATGAGATCATCATCATCAAGAAAAAAGAAATACATTAAGAAA 351
349 CCCAATGAGAGAACACAGACACATATTCGGGTCTGGAATGAAACTGTCTCAACCTG 408
352 CCCAATGAGAGAACACAGACACATATTCGGGTCTGGAATGAAACTGTCTCAACCTG 411
409 ACCCTTATGCGCCCTGGGTCTCTGCTCTGATATCTCTCTCTTATATGAGAGTGTG 468
412 ACCCTTATGCGCCCTGGGTCTCTGCTCTGATATCTCTCTCTTATATGAGAGTGTG 471
469 GGTATGAGTTCATGCTGCTGATCTGGAACCTTCTACCATTTGAGGAGTGCACCTTC 528
472 GGCATTAACCTTCACTGAGAGACCTGGTCTAGACCATCTGGGAGTGTGATCTC 531

529 AACATGTCATCATATGAGCATCTGTCTACGTATCCACAGAGAGACTCGCAG 588
532 AATATGTCATCATATGAGCATCTGTCTACGTATCCACAGAGAGACTCGCAG 591
589 ATCAGCATCTACGATCTCTTCTATCATCAGCGCTGTGGAGTATCTTGGCTTACATG 648
592 ATTAAGCATTTGCTGCTCTTCTTGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 651
649 CTCATATGATTTGCGAGCTCTTCTCCCTGGTGTGCTGAGGAGGAGGAGGAGGAGGAG 708
652 CTTTACATTTATTTTGTCTGATATCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 711
709 ACT 768
712 ACTTCT 771
769 TTCTACAAATTCATGCAACAAAAGTACCAGACAGACAAACAGAGAGATTTATCATGAG 828
772 TTTTACAAAGTATGTCACAAAGATATCGAGCTGCAAGAGAGGAGGAGATTTATGAA 831
829 ACAGAGGCTGACACCC-----TAAAGGCTTGAATGATGATGATGATGATGATGATGAT 879
832 CATGAGAGAGACAGAGCCATCTTCTAAGCTGMAATTTGAATGAGAGGAGAGTGTCAAT 891
880 TCCCATTTTCTAGATGGGAACCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 921
892 TCTCATGTTGAAATTTCTTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
922 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 981
952 GAT 1011
982 CCAGAGAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1041
1012 CCATATTAAGAAATATGAGCATTTATGATGATGATGATGATGATGATGATGATGATGAT 1071
1042 CAG 1101
1072 CAAAG 1131
1102 ATCTGAG 1161
1132 ATTTTAAAG 1191
1162 ACCGATGAGCTG---AGGACTTTTATTTCCAGAGCTCTCTCTCTCTCTCTCTCTCTCT 1218
1192 ACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1251
1219 TGCTGAG 1278
1252 TGCTGAG 1311
1279 AAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1338
1312 AACCTGCTGTTTGTGACTTCAGAACAGAGAGATGAGACAGACAAATGCTGGGTGATAT 1371
1339 GAGTTTACAG 1398
1372 GAATTTACTGAG 1431
1399 GGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1458
1432 GGTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1491
1459 GTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1518
1492 GTCAAGATCTTCTGAG 1542
1519 CCGTTGCTGAG 1578
1543 GTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1602
1579 GACCATGAG 1638

Db 1603 GACACGAGGCGATTTTACTTTTGAGGAACCTGTGACTCATGTGATGAGACANTGGC 1662
Qy 1639 GTTATGAGAGTCAAGGTTTGGCGACATCAGTCCCGGGGTACATCTGCTCCCTTT 1698
Db 1663 ATCATGTAGAGTAAAGATATGTGAGAACATCTGAGGCTCGGAAATGTATCTTCCTAT 1722
Qy 1699 AGCAGATGAGAGGACACCAAGGGTGGCGGTGAGGACTTTGAGACATATGAGGAG 1758
Db 1723 AAAACCATGGAAGGAGCTGCCAGAGGTGGAGGAGATTTGAGACACTGTGTGAGAG 1782
Qy 1759 TTGGAATTCAGAAATGATGAAACTGTGAAACCATAGGGTTAAATAGTAGATGAGAG 1818
Db 1783 CTCGAATTCAGAAATGATGAAATTTGAGAGATCATTTACATTTAGATATTTGACCGTGAG 1842
Qy 1819 GAATACGAAAGGCAAGAGATTTCTTCATTCCTGCTGTGAAACGAATGATGAGAGCT 1878
Db 1843 GAATATGAGAAAGAGTGCAGTTTCTCCCTGTCTGAGGAACCAAAATGATAGAGAGA 1902
Qy 1879 GGAATATCAG-----ATGTACAGACAGAGAGCTGACTATG 1914
Db 1903 GGAATGAAAGTGGCTTCAATTAACAGACGAATATGATGACAGCAGCCACTGACACG 1962
Qy 1915 GAAGAAGAGAGGCCAAGAGATAGCAGATGAGGAAACAGTATTTGGGTGAACACCC 1974
Db 1963 AAGAGAGAGAGAGAGGCGCATTTGAGAAATGGGGCCGCCATCCTGGAGAGACACACC 2022
Qy 1975 AAACTAGAAGTATCATTTGAGAGTCTATGAGTTCAGACTACGAGTACGGTGGACAAACTGATC 2034
Db 2023 AAGTTGGAAGTATCATTTGAGAAATCTATGATTCAGAGTACTGTGAGAAACTCATTT 2082
Qy 2035 AAGAAGACAAACCTGGCCCTTGTTGGGGACCCATTCCTGAGGAGACAGTTCAATGAGAG 2094
Db 2083 AAGAAGACAAACCTGGCCCTTGTTGGGGACTTAACAGCTGAGAGACAGATTCATTGAA 2142
Qy 2095 GCCATCACCGTCAGTCAGACAGGAGAGATGAGATGAGATGAATCCGGGAGAGAGAGCTG 2154
Db 2143 GCTATCAGTCTAGTGTGGGAGATGATGAGAGATGATGAGAGATGAGAGAGAGAGCTG 2202
Qy 2155 CCCTCCTGCTTTGACTACGTATGACACTTCTGACTGTCTTCTGGAAGTGTCTTTGCC 2214
Db 2203 CCCTCCTGTTGATGATGATGACACTTCTGACTGTCTGGAAGTGTCTTTGCC 2262
Qy 2215 TGTGTGCCCCCAGAGTACGACAGGCTGGGCTGCTGCGCTCTCCATCCCTCATC 2274
Db 2263 TTTGTCCTCCCTACGTAATGAGATGAGTGGCTGGGCTGTTCAATGTCTTCATCCCTCATG 2322
Qy 2275 ATTGCAATGCTACCGCCATCATTTGGGAGCTGGCCCTGCACTTGGCTGCAACATTTGGT 2334
Db 2323 ATTTGCTCTACGACGCTTTCATTTGAGAGCTGGCTTCCCACTTTGGCTGCAACATTTGGC 2382
Qy 2335 CTCGAAGATTCAGTACAGACTGTGTTTCTGTGGCATTTGGCACTCTGTCCAGATAGC 2394
Db 2383 CTGAAAGATTTGTGACTGATCGATCGTGTGCGCACTTGAACATCACTGGCAGACACA 2442
Qy 2395 TTTGGCAGCAAGAGTGTGCTCCCTCCAGAGATGATATGACAGAGCTTCCATTTGGCAAGTGTG 2454
Db 2443 TTTGGCAGCAAGAGTGTGCTCCCTCCAGAGATGATATGACAGAGCTTCCATTTAGTAACGTG 2502
Qy 2455 ACGGAGAGCAAGCGCTCAATGTCTTCTGGGATGCGGCTGAGCTGTGCTGAGCGGCGCC 2514
Db 2503 ACGGAGAGCAAGCGGCTGATGTCTTCTGGGATGCGGCTGTGCTGATGCTGCTGCTG 2562
Qy 2515 ATCTACTGGGCTCTGAGGAGAGAGATTCACGTGTGCGGCGGCACTGGGCTTCTCC 2574
Db 2563 ATCTACAGCAGCAGCAATGAGGAGAGTTCAAAGTGTCCCTGGCAGCTAGCTTCTCT 2622
Qy 2575 GTACACCTCTTACACATTTTGTGATGCTGATCAGGCTGTCTTGTACGAGAGCGG 2634
Db 2623 GTACACCTCTTACACATTTTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 2682
Qy 2635 CCGCACCTGGAGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2694

Db 2683 CCAGAAATGAGAGTGTGAGTGGGTGGGCCCCGAGCTGCCAAGCTCTCTCATCTGCTC 2742
Qy 2695 TTTGTGAGGCTGTGGCTCTCTACATACTTTTGGCAGACTAGAGGCTATTTGCTACATC 2754
Db 2743 TTTGTGCTCTATGTGCTCTTGTACATTTTCTCTCCTGAGAGGCTTACGCGACATA 2802
Qy 2755 AAGGCTCTTAA 2766
Db 2803 AAGGCTCTTAA 2814

Search completed: November 30, 2002, 12:02:11
Job time : 6126 secs

THIS PAGE BLANK (USPTO)